

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 24, 2004, 06:47:52 ; Search time 328 Seconds  
(without alignments)  
575.173 Million cell updates/sec

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Perfect score: 291  
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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 2438257 seqs, 184957644 residues  
Total number of hits satisfying chosen parameters: 4876514

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : Published Applications\_NA:\*  
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11: /cg2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cg2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
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18: /cg2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	291	100.0	285	9	US-09-829-381A-17	Sequence 17, Appl
2	291	100.0	288	9	US-09-759-584-58	Sequence 58, Appl
3	286	98.3	285	9	US-09-829-381A-16	Sequence 16, Appl
4	286	98.3	414	9	US-09-759-584-48	Sequence 48, Appl
5	286	98.3	414	13	US-10-006-252A-19	Sequence 19, Appl
6	281	96.6	403	9	US-09-732-561-13	Sequence 13, Appl
7	269	92.4	308	9	US-09-829-381A-5	Sequence 5, Appl
8	261	89.7	243	9	US-09-938-842A-2046	Sequence 2046, Ap
9	261	89.7	243	11	US-09-938-842A-2046	Sequence 1046, Ap
10	261	89.7	400	9	US-09-732-561-15	Sequence 15, Appl
11	261	89.7	400	9	US-09-887-576-607	Sequence 607, App
12	261	89.7	1616	9	US-09-732-561-21	Sequence 21, Appl
13	260	89.3	270	9	US-09-829-381A-14	Sequence 14, Appl
14	260	89.3	286	9	US-09-829-381A-12	Sequence 12, Appl
15	258	88.7	500	9	US-09-829-381A-9	Sequence 9, Appl
16	211	72.5	284	9	US-09-759-584-50	Sequence 50, Appl
17	201	69.1	306	9	US-09-829-381A-8	Sequence 8, Appl
18	166	57.0	373	9	US-09-770-696-283	Sequence 283, App
19	160	55.0	158	14	US-10-178-449A-34	Sequence 34, Appl
20	160	55.0	250	14	US-10-178-449A-36	Sequence 36, Appl
21	160	55.0	610	14	US-10-178-449A-29	Sequence 29, Appl
22	160	55.0	658	14	US-10-178-449A-7	Sequence 7, Appl
23	153	52.6	579	14	US-10-178-449A-31	Sequence 31, Appl
24	150	51.5	150	9	US-09-759-584-31	Sequence 31, Appl
25	150	51.5	529	14	US-10-178-449A-48	Sequence 48, Appl
26	149.5	51.4	470	14	US-10-178-213-88	Sequence 88, Appl
27	147	50.5	150	9	US-09-759-584-34	Sequence 34, Appl
28	146	50.2	439	14	US-10-178-449A-15	Sequence 15, Appl
29	146	50.2	457	14	US-10-178-449A-13	Sequence 13, Appl
30	146	50.2	458	14	US-10-178-449A-21	Sequence 21, Appl
31	146	50.2	460	14	US-10-178-449A-17	Sequence 17, Appl
32	146	50.2	461	14	US-10-178-449A-46	Sequence 46, Appl
33	146	50.2	463	14	US-10-178-449A-9	Sequence 9, Appl
34	146	50.2	464	14	US-10-178-449A-19	Sequence 19, Appl
35	146	50.2	472	14	US-10-178-449A-23	Sequence 23, Appl
36	146	50.2	603	14	US-10-178-449A-11	Sequence 11, Appl
37	145	49.8	150	9	US-09-759-584-33	Sequence 33, Appl
38	145	49.8	460	14	US-10-178-449A-3	Sequence 3, Appl
39	145	49.8	503	14	US-10-178-449A-25	Sequence 25, Appl
40	138	47.4	499	14	US-10-178-449A-27	Sequence 27, Appl
41	138	47.4	517	14	US-10-178-449A-36	Sequence 36, Appl
42	136.5	46.9	147	9	US-09-759-584-4	Sequence 4, Appl
43	109.5	37.6	564	9	US-09-777-347-1	Sequence 1, Appl
44	109.5	37.6	3528	9	US-09-777-347-2	Sequence 2, Appl
45	103.5	35.6	476	14	US-10-178-213-127	Sequence 127, App

## ALIGNMENTS

RESULT 1  
US-09-829-381A-17  
Sequence 17, Application US/09829381A  
Patent No. US20020144306A1

GENERAL INFORMATION:  
APPLICANT: Liang, Jihong

Shah, Dilip M.  
Wu, Yonnie S.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSES: Charles E. Cohen, Monsanto Company, B44F  
STREET: 700 Chesterfield Village Parkway No. US20020144306A1th

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/09/829,381A  
APPLICATION NUMBER: US/09/829,381A  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/103,489  
FILING DATE: 1998-06-24  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-829-381A-17

Alignment Scores:  
Pred. No.: 1,38e-30 Length: 285  
Score: 291.00 Matches: 47  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

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QY 1 GlnlysluCyS\*\*\*ArpProSer\*\*\*ThrTpSerGlyValCyS\*\*\*AsnAsnAsnAla 20  
Db 118 CAAAGTGTGCGAAGGCGCATCGTGTGCGAGCTCTCGGAAACATTAACGCA 177

QY 21 CyslyAsnGlnCyS11eArGleuGlnlySAlaArGh1eGlySerCySAsnTyrr\*\*\*Phe 40  
Db 178 TGCAGAAACCATGATGATGACTCGAAGGCGCATGATCTTGCACTTACTTTC 237

QY 41 ProAlaHisIlyeCyS11eCyS1TyrrPheProCyS 51  
Db 238 CCAGCTCACAGTGCATCTGCTACTTTCATTC 270

RESULT 2  
US-09-759-584-58  
Sequence 58, Application US/09759584  
Patent No. US20010014732A1  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMUDE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH B.  
APPLICANT: TERRAS, FRANKY R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARBY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/759,584  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/377,667  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-861-3000  
TELEFAX: 202-822-0944  
INFORMATION FOR SEQ ID NO: 58:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 288 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 43..282  
US-09-759-584-58

Alignment Scores:  
Pred. No.: 1,41e-30 Length: 288  
Score: 291.00 Matches: 47  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0

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Db 130 CAAAGTGTGCGAAGGCGCATGCGATGCTGTGGAACATTAACGCA 189

QY 21 CyslyAsnGlnCyS11eArGleuGlnlySAlaArGh1eGlySerCySAsnTyrr\*\*\*Phe 40  
Db 190 TGCAGAAACCATGATGATGACTCGAAGGCGCATGATCTTGCACTTACTTTC 249

QY 41 ProAlaHisIlyeCyS11eCyS1TyrrPheProCyS 51  
Db 250 CCAGCTCACAGTGCATCTGCTACTTTCCTTGT 282

RESULT 3  
US-09-829-381A-16  
Sequence 16, Application US/09829381A  
Patent No. US20020144306A1  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, B44F  
STREET: 700 Chesterfield Village Parkway No. US20020144306A1ch  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

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/
/ APPLICATION NUMBER: US/09/829,381A
/ FILING DATE: 09-Apr-2001
/ CLASSIFICATION: <Unknown>
/
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 09/103,489
/ FILING DATE: 1998-06-24
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Cohen, Charles E.
/ REGISTRATION NUMBER: 34,565
/ REFERENCE/DOCKET NUMBER: 38-21 (10700)A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (314) 537-6047
/ TELEFAX: (314) 537-6047
/
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 285 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "synthetic DNA"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-829-381A-16

Alignment Scores:
Pred. No.: 6,67e-30 Length: 285
Score: 286.00 Matches: 46
Percent Similarity: 98.04% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-16 (1-285)

QY 1 GlnlysluCyS**AqProSer**ThTTPSerGlyValCyS**AaAsnAsnAla 20
Db 118 CAAAGATTGTGCGAGAGCCATCAGGACTTGGTCAGAGTCTGGCGAACAACGCA 177

QY 21 CyslysaSngInCysIleArgSleuGluValArgHisGlySerCysAsnTyR**Phe 40
Db 178 TCGAAGAACCAAGATCAACCTCGAAGAGCAGGCGATGATCTTGCAACTACGCTTC 237

QY 41 ProAlaHislyCySsileCySTyRPhProCyS 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTTCATGCG 270

RESULT 4
US-09-759-584-48
/ Sequence 48, Application US/09759584
/ Patent No. US20010014732A1
/ GENERAL INFORMATION:
/ APPLICANT: BROEKERT, WILLEM F.
/ APPLICANT: CAMMUE, BRUNO P.A.
/ APPLICANT: OSEBORN, RUPERT W.
/ APPLICANT: REES, SARAH B.
/ APPLICANT: TERRAS, FRANKY R.G.
/ APPLICANT: VANDERLEYDEN, JOZEF
/ TITLE OF INVENTION: BIOCIDAL PROTEINS
/ NUMBER OF SEQUENCES: 59
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: CUSHMAN DABRY & CUSHMAN
/ STREET: 1100 NEW YORK AVENUE, N.W.
/ CITY: WASHINGTON
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20005
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/759,584
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/
/ FILING DATE:
/ CLASSIFICATION:
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 08/377,687
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: KOKULIS, PAUL N.
/ REGISTRATION NUMBER: 16,773
/ REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-861-3000
/ TELEFAX: 202-822-0944
/
/ INFORMATION FOR SEQ ID NO: 48:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 414 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: both
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 16..255
US-09-759-584-48

Alignment Scores:
Pred. No.: 1.13e-29 Length: 414
Score: 286.00 Matches: 46
Percent Similarity: 98.04% Conservative: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-759-584-48 (1-414)

QY 1 GlnlysluCyS**AqProSer**ThTTPSerGlyValCyS**AaAsnAsnAla 20
Db 103 CAGAAGTTGTGCGAAGCCCAAGTGCAGATGTCAGAGATCTGTGGAACAATTAACGCA 162

QY 21 CyslysaSngInCysIleArgSleuGluValArgHisGlySerCysAsnTyR**Phe 40
Db 163 TCGAAGAACCAAGATCAACCTCGAAGAGCAGGCGATGATCTTGCAACTACGCTTC 222

QY 41 ProAlaHislyCySsileCySTyRPhProCyS 51
Db 223 CCAGCTCACAAGTGCATCTGCTACTTTCATGCG 255

RESULT 5
US-10-006-252A-19
/ Sequence 19, Application US/10006252A
/ Publication No. US20020152498A1
/ GENERAL INFORMATION:
/ APPLICANT: De Samblanx, Genevieve
/ APPLICANT: Broekaert, Willem
/ APPLICANT: Rees, Sarah
/ TITLE OF INVENTION: Antifungal Proteins
/ FILE REFERENCE: SYN-034DV
/ CURRENT APPLICATION NUMBER: US/10/006,252A
/ PRIOR FILING DATE: 2001-12-04
/ PRIOR APPLICATION NUMBER: 09/077,951
/ PRIOR FILING DATE: 1998-06-10
/ PRIOR APPLICATION NUMBER: GB 9525474.4
/ PRIOR FILING DATE: 1995-12-13
/ PRIOR APPLICATION NUMBER: PCT/GB96/03065
/ PRIOR FILING DATE: 1996-12-12
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 19
/ LENGTH: 414
/ TYPE: DNA
/ ORGANISM: Raphanus sativus
US-10-006-252A-19

Alignment Scores:
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Pred. No.: 1.13e-29 Length: 414  
 Score: 286.00 Matches: 46  
 Percent Similarity: 98.04% Conservative: 4  
 Best Local Similarity: 90.20% Mismatches: 1  
 Query Match: 98.28% Indels: 0  
 DB: 13 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-10-006-252A-19 (1-414)

QY 1 GlnLysLeuCys\*\*ArgProSer\*\*ThrTrpSerGlyValCys\*\*AsnAsnAsnAla 20  
 Db 103 CAGAGGTGTGCGAAGGCCAAGTGGACATGTCAGAGCTGTGGAAACAATAACGCA 162  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTrp\*\*\*Phe 40  
 Db 163 TGCAGAGTGTGCGAAGGCCAAGTGGACATGTCAGAGCTGTGGAAACAATAACGCA 222  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 Db 223 CCAGCTCAACAAGTGTATCTGCTACTTCCCTGT 255

## RESULT 6

US-09-732-561-13

Sequence 13, Application US/09732561

Patent No. US20020035738A1

GENERAL INFORMATION:

APPLICANT: Thomma, Bart

APPLICANT: Terras, Franky

APPLICANT: Penninckx, Iris

APPLICANT: Mannere, John

APPLICANT: Kazan, Kemal

APPLICANT: Broekaert, Willem

TITLE OF INVENTION: Plant Protection Method

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESSES:

ADDRESSEE: ZENECA Ag Products

STREET: 1800 Concord Pike

CITY: Wilmington

STATE: DE

COUNTRY: USA

ZIP: 19850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/732,561

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/202,638

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB97/01672

FILING DATE: 20-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Hobenschutz, Liza D.

REGISTRATION NUMBER: 33,712

REFERENCE/DOCKET NUMBER: PPD 50165/UST

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302) 886-1699

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 403 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

STRAIN: PDF 1.1

US-09-732-561-13

Alignment Scores:  
 Pred. No.: 5.23e-29 Length: 403  
 Score: 281.00 Matches: 45  
 Percent Similarity: 98.04% Conservative: 5  
 Best Local Similarity: 88.24% Mismatches: 1  
 Query Match: 96.56% Indels: 0  
 DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-732-561-13 (1-403)

QY 1 GlnLysLeuCys\*\*ArgProSer\*\*ThrTrpSerGlyValCys\*\*AsnAsnAsnAla 20  
 Db 113 CAGAGGTGTGCGAAGGCCAAGTGGACATGTCAGAGCTGTGGAAACAATAACGCA 172  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTrp\*\*\*Phe 40  
 Db 173 TGCAGAGTGTGCGAAGGCCAAGTGGACATGTCAGAGCTGTGGAAACAATAACGCA 232  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 Db 233 CCAGCTCAACAAGTGTATCTGCTACTTCCCATGT 265

## RESULT 7

US-09-829-381A-5

Sequence 5, Application US/09829381A

Patent No. US20020144306A1

GENERAL INFORMATION:

APPLICANT: Liang, Jihong

APPLICANT: Shan, Dilip K.

APPLICANT: Wu, Yonnie S.

APPLICANT: Rosenberger, Cindy A.

TITLE OF INVENTION: Antifungal Polypeptide and Methods for

Controlling Plant Pathogenic Fungi

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF

STREET: 700 Chesterfield Village Parkway No. US20020144306A1ch

CITY: St. Louis

STATE: Missouri

COUNTRY: USA

ZIP: 63198

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/829,381A

FILING DATE: 09-Apr-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/103,489

FILING DATE: 1998-06-24

ATTORNEY/AGENT INFORMATION:

NAME: Cohen, Charles E.

REGISTRATION NUMBER: 34,565

REFERENCE/DOCKET NUMBER: 38-21 (10700)A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (314) 537-6224

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 308 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-829-381A-5

## Alignment Scores:

Pred. No.: 1.56e-27 Length: 308  
 Score: 269.00 Matches: 43

Percent Similarity: 94.12% Conservative: 5  
Best Local Similarity: 84.31% Mismatches: 3  
Query Match: 92.44% Indels: 0  
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-5 (1-308)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAsnAla 20  
Db 156 CGGAAGTTGTGCGAGAGTCCAAAGTGAACATGCTCAGGCGGTGTGTGGAAACAAATGCT 215  
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
Db 216 TGAAGAATCAGTGCATTAAACCTTGAAGGAGCNCAGCATGATCTTGCACATGATGCTTC 275  
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
Db 276 CCAGCTCACAAGTGCATATGCTACTTCCCTGT 308

RESULT 8

US-09-938-842A-2046  
; Sequence 2046, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SRIPL300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2046  
; LENGTH: 243  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2046

Alignment Scores:  
Pred. No.: 1.38e-26 Length: 243  
Score: 261.00 Matches: 41  
Percent Similarity: 94.12% Conservative: 7  
Best Local Similarity: 80.39% Mismatches: 3  
Query Match: 89.69% Indels: 0  
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-938-842A-2046 (1-243)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAsnAla 20  
Db 88 CAGAAGTTGTGCGAGAAGCCAAAGTGGGACATGCTCAGGCGGTGTGGGAAACAGTAATGCA 147  
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
Db 148 TGAAGAATCAGTGCATTAAACCTTGAAGGAGCNCAGCATGATCTTGCACATGATGCTTC 207

RESULT 9

US-09-938-842A-2046  
; Sequence 2046, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SRIPL300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2046  
; LENGTH: 243  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2046

Alignment Scores:  
Pred. No.: 1.38e-26 Length: 243  
Score: 261.00 Matches: 41  
Percent Similarity: 94.12% Conservative: 7  
Best Local Similarity: 80.39% Mismatches: 3  
Query Match: 89.69% Indels: 0  
DB: 11 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-938-842A-2046 (1-243)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAsnAla 20  
Db 88 CAGAAGTTGTGCGAGAAGCCAAAGTGGGACATGCTCAGGCGGTGTGGGAAACAGTAATGCA 147  
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
Db 148 TGAAGAATCAGTGCATTAAACCTTGAAGGAGCNCAGCATGATCTTGCACATGATGCTTC 207  
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
Db 208 CCAGCACAAGTGTATCTGTTACCTCCATGT 240

RESULT 10

US-09-732-561-15  
; Sequence 15, Application US/09732561  
; Patent No. US20020035738A1  
; GENERAL INFORMATION:

; APPLICANT: Thoma, Bart  
; APPLICANT: Terras, Franky  
; APPLICANT: Penninckx, Iris  
; APPLICANT: Manners, John  
; APPLICANT: Kazan, Kemal  
; APPLICANT: Broekaert, Willem  
; TITLE OF INVENTION: Plant Protection Method  
; NUMBER OF SEQUENCES: 24  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ZENECA Ag Products  
; STREET: 1800 Concord Pike  
; CITY: Wilmington  
; STATE: DE  
; COUNTRY: USA  
; ZIP: 19850

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/732,561  
; FILING DATE:  
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB97/01672
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; STRAIN: Ppfl.2
US-09-732-561-15

Alignment Scores:
Pred. No.: 2,79e-26 Length: 400
Score: 261.00 Matches: 41
Percent Similarity: 94.12% Conservative: 7
Best Local Similarity: 80.39% Mismatches: 3
Query Match: 89.69% Indels: 0
DB: Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-732-561-15 (1-400)

QY 1 GlnLysLeuCyS***ArgProSer***ThrTpSerGlyValCys***AsnAsnAsnAla 20
Db 119 CAGAAGTTGTGGAGAGCAAGTGGACATGTCAGGGGTTTGGGAAACAGTAATGCA 178
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 179 TGCAGAATCAGTCATTAACTTGAAGAGGCAACATGATCATGCAACTATGTCCTTC 238

RESULT 11
US-09-887-576-607
; Sequence 607, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression
; FILE REFERENCE: 1360, 001US1
; CURRENT APPLICATION NUMBER: US/09/887,576
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,848
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/214,087
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/258,692
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 875
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 607
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(400)
; OTHER INFORMATION: n = A,T,C or G
US-09-887-576-607

Alignment Scores:
Pred. No.: 2,79e-26 Length: 400
Score: 261.00 Matches: 41
Percent Similarity: 94.12% Conservative: 7
Best Local Similarity: 80.39% Mismatches: 3
Query Match: 89.69% Indels: 0
DB: Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-887-576-607 (1-400)

QY 1 GlnLysLeuCyS***ArgProSer***ThrTpSerGlyValCys***AsnAsnAsnAla 20
Db 119 CAGAAGTTGTGGAGAGCAAGTGGACATGTCAGGGGTTTGGGAAACAGTAATGCA 178
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 179 TGCAGAATCAGTCATTAACTTGAAGAGGCAACATGATCATGCAACTATGTCCTTC 238

RESULT 12
US-09-732-561-21
; Sequence 21, Application US/09732561
; Patent No. US20020035738A1
; GENERAL INFORMATION:
; APPLICANT: Thomas, Bart
; APPLICANT: Terras, Franky
; APPLICANT: Penninckx, Iris
; APPLICANT: Manners, John
; APPLICANT: Kazan, Kemal
; APPLICANT: Broekert, Willem
; TITLE OF INVENTION: Plant Protection Method
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZENECA Ag Products
; STREET: 1800 Concord Pike
; CITY: Wilmington
; STATE: DE
; COUNTRY: USA
; ZIP: 19850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/732,561
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/202,638
; FILING DATE:
; PRIOR APPLICATION DATA: PCT/GB97/01672
; APPLICATION NUMBER:
; FILING DATE: 20-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Hohenschutz, Liza D.
; REGISTRATION NUMBER: 33,712
; REFERENCE/DOCKET NUMBER: PPD 50165/UST
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (302) 886-1699
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1616 base pairs
; TYPE: nucleic acid

```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; STRAIN: Arabidopsis PDF1.2 gene
; INDIVIDUAL ISOLATE: DNA sequence Figure 14
US-09-732-561-21

Alignment Scores:
Pred. No.: 1,99e-25 Length: 1616
Score: 261.00 Matches: 41
Percent Similarity: 94.12% Conservative: 7
Best Local Similarity: 80.39% Mismatches: 3
Query Match: 89.69% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-732-561-21 (1-1616)

QY 1 GlnYsLeuCyS***ArgProSer***ThrTpSerGlyValCyS***AsnAsnAla 20
Db 1412 CAGAGTGTGCGAGAACCAAGTGGACATGGTCAGGGGTTTCGGAAACAGTAATGCA 1471

QY 21 CysYsAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 1472 TGCAGAAATCAGTCGATTACCTCGAAGAGCCAAACATGGATCATGCAACTATGTCTTC 1531

QY 41 ProlahisYsCysIleCysTyrPheProCys 51
Db 1532 CCAGCACAAAGTGTATCTGTACGTCCCATGT 1564

RESULT 13
US-09-829-381A-14
; Sequence 14, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip M.
; Wu, Yennie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 14:
; LENGTH: 270 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-829-381A-14

Alignment Scores:
Pred. No.: 2,2e-26 Length: 270
Score: 260.00 Matches: 40
Percent Similarity: 94.00% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 3
Query Match: 89.35% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-14 (1-270)

QY 2 LysLeuCyS***ArgProSer***ThrTpSerGlyValCyS***AsnAsnAlaCyS 21
Db 109 AGTGTGGCGAGAGACCAAGTGGACATGGTCAGAGTTTGGGACACACATGCAATGC 168

QY 22 LysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***PhePro 41
Db 169 AGGAACCAATGAGAAACCTTGAAGAGCAGAACACGATCTTGCACACTATGTCTTCCA 228

QY 42 AlaHisLysCysIleCysTyrPheProCys 51
Db 229 GGTCAACAAATGATTGTGTACTTCCCATGT 258

RESULT 14
US-09-829-381A-12
; Sequence 12, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Shah, Dilip M.
; Wu, Yennie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
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US-09-829-381A-12
Alignment Scores:
Pred. No.: 2.38e-26 Length: 286
Score: 260.00 Matches: 40
Percent Similarity: 94.00% Conservative: 7
Best Local Similarity: 80.00% Mismatches: 3
Query Match: 89.35% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-12 (1-286)
QY 2 LysLeuCyS***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAlaCys 21
Db 117 AGTTGTCGGAGACCAAGTGGACATGTCAGAGTTTGGGACACACATGCAATGC 176
QY 22 LysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***PhePro 41
Db 177 AGGAACCAATGCAGAAACCTTGAAGAGCAGACACGATCTTGCAACTATGTTCCCA 236
QY 42 AlaHisLysCysIleCysTyrPheProCys 51
Db 237 GCTCAAAATGATTGTTTACTTCCCATGT 266

RESULT 15
US-09-829-381A-9
; Sequence 9, Application US/09829381A
; Patent No. US20020144306A1
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; Wu, Yonnie S.
; Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BBAF
; STREET: 700 Chesterfield Village Parkway No. US20020144306A1th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/829,381A
; FILING DATE: 09-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-829-381A-9
Alignment Scores:
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```
Pred. No.: 9.81e-26 Length: 500
Score: 258.00 Matches: 40
Percent Similarity: 92.16% Conservative: 7
Best Local Similarity: 78.43% Mismatches: 4
Query Match: 88.66% Indels: 0
DB: 9 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381A-9 (1-500)
QY 1 GlnLysLeuCyS***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAla 20
Db 156 CGGAAGTTGTCGAGAGTCCAAGTGGAAACATGGTCAGCGTGTGGGAATAATAACGCA 215
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 216 TGCAGAACCAATGCGAAACCTTGAAGAGCAGACACGATCTTGCAACTATGTTCTTC 275
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 276 CCAGCTCACAAATGTTTACTTCCCATGT 308

Search completed: March 24, 2004, 09:17:33
Job time : 342 secs
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 24, 2004, 05:43:48 ; Search time 3189 Seconds

(without alignments)

477,570 Million cell updates/sec

Title: SEQ9-X-AT-5-9-16-39

Perfect score: 291

Sequence: 1 QKLCXSPSXTWGVCXNNNA.....RGGSCNYXFPAAHKICVYPC 51

Scoring table: BLOSUM62DX

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO.spool/ROBINSON10006252/tunat\_23032004\_112103\_24808/app\_query.fasta\_1.19  
-DB=EST -OPWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62DX -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -NINLEN=0 -MAXLEN=2000000000  
-USER=ROBINSON10006252@cgn\_1\_3437\_@tunat\_23032004\_112103\_24808 -NCPU=6  
-ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hcc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hcc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_eston:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vit:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	291	100.0	409	14	CD832294	CD832294 BN40.062L
2	291	100.0	425	14	CD834852	CD834852 BN45.043G
3	291	100.0	427	14	CD833613	CD833613 BN40.067P
4	291	100.0	449	14	CD833047	CD833047 BN40.065M
5	291	100.0	457	14	CD831226	CD831226 BN40.058J
6	291	100.0	473	14	CD834995	CD834995 BN45.043O
7	291	100.0	476	14	CD833784	CD833784 BN45.040I
8	291	100.0	476	14	CD834092	CD834092 BN45.040I
9	291	100.0	481	14	CD833924	CD833924 BN45.040A
10	291	100.0	482	14	CD833627	CD833627 BN45.041A
11	291	100.0	523	14	CD833661	CD833661 BN45.041C
12	291	100.0	543	14	CD828840	CD828840 BN40.040A
13	291	100.0	646	14	CD829429	CD829429 BN40.042B
14	291	100.0	762	28	EZ517729	EZ517729 BOMSG6TF
15	287	98.6	522	14	CD833938	CD833938 BN45.040A
16	287	98.6	543	14	CD829085	CD829085 BN40.041A
17	286	98.3	408	14	CD833779	CD833779 BN45.041I
18	286	98.3	409	14	CD834090	CD834090 BN45.040I
19	286	98.3	418	14	CD832625	CD832625 BN40.064A
20	286	98.3	419	14	CD834168	CD834168 BN45.040N
21	286	98.3	420	14	CD833944	CD833944 BN45.040B
22	286	98.3	421	14	CD826491	CD826491 BN45.064A
23	286	98.3	421	14	CD831111	CD831111 BN40.058A
24	286	98.3	421	14	CD833977	CD833977 BN45.040D
25	286	98.3	422	14	CD833983	CD833983 BN45.040D
26	286	98.3	426	14	CD827413	CD827413 BN25.067G
27	286	98.3	438	14	CD831294	CD831294 BN40.058N
28	286	98.3	438	14	CD831479	CD831479 BN40.059J
29	286	98.3	446	14	CD834068	CD834068 BN45.040H
30	286	98.3	447	14	CD832592	CD832592 BN40.063O
31	286	98.3	450	14	CD834611	CD834611 BN45.042H
32	286	98.3	452	14	CD832071	CD832071 BN40.061O
33	286	98.3	453	14	CD834008	CD834008 BN45.040E
34	286	98.3	458	14	CD834994	CD834994 BN45.043O
35	286	98.3	470	14	CD831680	CD831680 BN40.060H
36	286	98.3	480	14	CD828332	CD828332 BN25.070H
37	286	98.3	543	14	CD830628	CD830628 BN40.046D
38	286	98.3	553	14	CD831014	CD831014 BN40.047K
39	286	98.3	803	28	BH458392	BH458392 BOGW636TF
40	282	96.9	457	14	CD831392	CD831392 BN40.059D
41	281	96.6	318	9	AA713157	AA713157 32717 Lam
42	281	96.6	421	9	AV816118	AV816118 AV816118
43	281	96.6	422	9	AV787956	AV787956 AV787956
44	280	96.2	448	14	CD837568	CD837568 BN45.052M
45	277	95.2	421	14	CD837517	CD837517 BN45.052I

ALIGNMENTS

RESULT 1	CD832294	409 bp	mRNA	linear	EST 10-JUL-2003			
LOCUS	BN40.062L22F011227	BN40	Brassica napus	cdna clone	BN40062L22, mRNA			
DEFINITION	sequence.							
ACCESSION	CD832294							
VERSION	CD832294.1	GI:32514234						
KEYWORDS	EST.							
SOURCE	Brassica napus (rape)							
ORGANISM	Brassica napus							
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.								

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/tissue_type="seed"
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ORIGIN

Alignment Scores:
Pred. No.:      8,1e-23      Length:      425
Score:          291.00      Matches:     47
Percent Similarity: 100.00%      Conservative: 4
Best Local Similarity: 92.16%      Mismatches:  0
Query Match:    100.00%      Indels:      0
DB:             14          Gaps:        0

SEQ3-X-AT-5-9-16-39 (1-51) x CD834852 (1-425)

QY      1  GlnLyLeuCys***ArgProSer***ThrTTrSerGlyValCys***AsnAsnAsnAla 20
Db      136  CAGAAGCTGTGCAGAGGCGCAAGTGAACGTGTGTGAGGAGTCTGTGGAAACAATAATGCA 195

QY      21  CysLyAsnGlnCysIleArgLeuGluLyAlaArgHisGlySerCysAsnTyr***Phe 40
Db      196  TGAAGAATCAGTGTGATTCGACTAGAGAAGACGACATGCACTTGTGCAACTATGCTTC 255

QY      41  ProAlaHisLyScysIleCysTyrPheProCys 51
Db      256  CCAGCTCACAGTGCATCTGCTACTTCCCTTGT 288

RESULT 3
CD833613
LOCUS   CD833613      427 bp      mRNA      linear      EST 10-JUL-2003
DEFINITION  BN40.067P16F011228 BN40 Brassica napus cDNA clone BN40067P16, mRNA
sequence.
CD833613
CD833613.1  GI:32515553
EST.
SOURCE    Brassica napus (rape)
ORGANISM  Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 427)
AUTHORS   Genoplante.
TITLE     Genoplante, a major partnership french program in plant genomics
JOURNAL   Unpublished (2003)
COMMENT   Contact: Genoplante
          Genoplante
          93, rue Henri Rochefort 91025 EVRY CEDEX France
          Tel: 33 1 69 47 54 00
          Fax: 33 1 69 47 54 10
          This sequence has been generated in the framework of the french
          plant genomics programme 'Genoplante' (http://www.genoplante.com
          and http://genoplante-info.inbioigen.fr).

FEATURES             source
     source           1..427
                        /organism="Brassica napus"
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ORIGIN

Alignment Scores:
Pred. No.:      8,16e-23      Length:      427
Score:          291.00      Matches:     47
Percent Similarity: 100.00%      Conservative: 4
Best Local Similarity: 92.16%      Mismatches:  0
Query Match:    100.00%      Indels:      0
DB:             14          Gaps:        0

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TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

## FEATURES

source  
1..473  
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## ORIGIN

Alignment Scores: 9.44e-23 Length: 473  
Pred. No.: 291.00 Matches: 47  
Score: 291.00  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD834995 (1-473)

QY 1 GlnLysLeuCyS\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCyS\*\*\*AsnAsnAla 20  
DB 156 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTTGTGGAAACAATAATGCG 215  
QY 21 CysLysAsnGlnCysIleAargLeuGlnLysAlaAargHisGlySerCysAsnTy\*\*\*Phe 40  
DB 216 TGTAAAGATCATGTCATTCGATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 275  
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
DB 276 CCAGCTCACAGTGTATCTGCTATTTCCTTGT 308

## RESULT 7

CD833784  
LOCUS BN45.001122F010914 BN45 Brassica napus cDNA clone BN45001122, mRNA  
DEFINITION sequence.  
ACCESSION CD833784  
VERSION CD833784.1 GI:32515724  
KEYWORDS EST.  
SOURCE Brassica napus (rape)

ORGANISM  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 476)

## REFERENCE

AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

## FEATURES

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Alignment Scores: 9.53e-23 Length: 476  
Pred. No.: 291.00 Matches: 47  
Score: 291.00  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD833784 (1-476)

QY 1 GlnLysLeuCyS\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCyS\*\*\*AsnAsnAla 20  
DB 157 CAGAAAGTTGTGTGAGAGCCAAAGTGGACATGTCAGGAGTTTGTGGAAACAATAATGCG 216  
QY 21 CysLysAsnGlnCysIleAargLeuGlnLysAlaAargHisGlySerCysAsnTy\*\*\*Phe 40  
DB 217 TGTAAAGATCATGTCATTCGATTCGATTCGAGAAAGCAGCATGATCTTGCAACTATGCTTC 276  
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
DB 277 CCAGCTCACAGTGTATCTGCTATTTCCTTGT 309

## RESULT 8

CD834092  
LOCUS BN45.040123F011018 BN45 Brassica napus cDNA clone BN45040123, mRNA  
DEFINITION sequence.  
ACCESSION CD834092  
VERSION CD834092.1 GI:32516032  
KEYWORDS EST.  
SOURCE Brassica napus (rape)

ORGANISM  
Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 476)

## REFERENCE

AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

## FEATURES

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/clone="BN45040123"  
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## ORIGIN

Alignment Scores: 9.53e-23 Length: 476  
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Score: 291.00  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD834092 (1-476)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAsnAla 20  
 Db 157 CAGAAGTTGTGTGAGAGGCCAAGTGGGACATGTCAGGAGTTTGTGGAAACAATAATGCG 216  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 Db 217 TGTAAAGATCAGTGCATTCGACTTGAGAAAGACACATGGATCTTGGCAACTATGTCTTC 276  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 Db 277 CCAGCTCACAAAGTGTATCTGCTATTTCCCTTGT 309

RESULT 9  
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 LOCUS DEFINITION EN45.040A03F011018 BN45 Brassica napus cDNA clone BN45040A03, mRNA  
 sequence.  
 ACCESSION CD833924  
 VERSION CD833924.1 GI:32515864  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 481)  
 Genoplate.  
 Genoplate, a major partnership french program in plant genomics  
 Unpublished (2003)  
 CONTACT: Genoplate  
 Genoplate  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplate' (<http://www.genoplate.com>  
 and <http://genoplate-info.infobiogen.fr>).  
 and <http://genoplate-info.infobiogen.fr>).  
 Location/Qualifiers  
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 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

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 Db 156 CAGAAGTTGTGTGAGAGGCCAAGTGGGACATGTCAGGAGTTTGTGGAAACAATAATGCG 215  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 Db 216 TGTAAAGATCAGTGCATTCGACTTGAGAAAGACACATGGATCTTGGCAACTATGTCTTC 275  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 Db 276 CCAGCTCACAAAGTGTATCTGCTATTTCCCTTGT 308

RESULT 10  
 CD833627

LOCUS CD833627 482 bp mRNA linear EST 10-JUL-2003  
 DEFINITION EN45.001A11F010914 BN45 Brassica napus cDNA clone BN45001A11, mRNA  
 sequence.  
 ACCESSION CD833627  
 VERSION CD833627.1 GI:32515567  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 482)  
 Genoplate.  
 Genoplate, a major partnership french program in plant genomics  
 Unpublished (2003)  
 CONTACT: Genoplate  
 Genoplate  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplate' (<http://www.genoplate.com>  
 and <http://genoplate-info.infobiogen.fr>).  
 and <http://genoplate-info.infobiogen.fr>).  
 Location/Qualifiers  
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 /tissue\_type="seed"  
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 Alignment Scores:  
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 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 14 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x CD833627 (1-482)  
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 Db 157 CAGAAGTTGTGTGAGAGGCCAAGTGGGACATGTCAGGAGTTTGTGGAAACAATAATGCG 216  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 Db 217 TGTAAAGATCAGTGCATTCGACTTGAGAAAGACACATGGATCTTGGCAACTATGTCTTC 276  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 Db 277 CCAGCTCACAAAGTGTATCTGCTATTTCCCTTGT 309

RESULT 11  
 CD833661 523 bp mRNA linear EST 10-JUL-2003  
 LOCUS DEFINITION EN45.001C04F010914 BN45 Brassica napus cDNA clone BN45001C04, mRNA  
 sequence.  
 ACCESSION CD833661  
 VERSION CD833661.1 GI:32515601  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 523)  
 Genoplate.  
 Genoplate, a major partnership french program in plant genomics  
 Unpublished (2003)





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 24, 2004, 03:45:35 ; Search time 405 Seconds  
(without alignments)  
534.958 Million cell updates/sec

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Perfect score: 291  
Sequence: 1 QKLCXRPSTWGVXNNNA.....RHGSCNYXPPAHKICICYPFC 51

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 337863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: geneseqn2003bs:\*  
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10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	291	100.0	261	2 AAQ38652	AaQ38652 Rs-APP2 C
2	291	100.0	288	2 AAQ70130	AaQ70130 Antimicro
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4	291	100.0	437	3 AAZ99331	Aaz99331 DNA encod
5	291	100.0	443	3 AAZ99330	Aaz99330 DNA encod
6	291	100.0	446	3 AAZ99329	Aaz99329 DNA encod
7	291	100.0	449	3 AAAS3190	AaAS3190 Raphanus
8	291	100.0	485	3 AAZ99333	Aaz99333 DNA encod

9	291	100.0	485	3 AAZ99335	Aaz99335 DNA encod
10	291	100.0	485	3 AAZ99337	Aaz99337 DNA encod
11	291	100.0	488	3 AAZ99338	Aaz99338 DNA encod
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13	291	100.0	534	3 AAZ51396	Aaz51396 Portion o
14	291	100.0	534	3 AAZ99327	Aaz99327 DNA encod
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19	291	100.0	1093	3 AAZ99334	Aaz99334 DNA encod
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21	286	98.3	414	2 AAQ38650	AaQ38650 Rs-APP1 C
22	286	98.3	414	2 AAQ70128	AaQ70128 Antimicro
23	286	98.3	414	2 AA772333	Aa772333 Raphanus
24	286	98.3	414	2 AAT68696	Aat68696 Radish an
25	286	98.3	426	9 ADC51223	AdC51223 Brassica
26	281	96.6	243	7 ADA68378	Ada68378 Arabidops
27	281	96.6	403	2 AAV10632	AaV10632 A. thalia
28	269	92.4	308	2 AAT94577	Aat94577 Cloned 5,
29	261	89.7	243	6 ABZ14241	Abz14241 Arabidops
30	261	89.7	243	7 ABZ42136	Abz42136 Arabidops
31	261	89.7	400	2 AAV10633	AaV10633 A. thalia
32	261	89.7	1616	2 AAV10646	AaV10646 A. thalia
33	260	89.3	270	2 AAT94582	Aat94582 Amplified
34	260	89.3	286	2 AAT94574	Aat94574 Alyssum s
35	260	89.3	481	2 AAT99289	Aat99289 Alyssum s
36	259	89.0	243	6 ABQ82690	Abq82690 Wasabia j
37	259	89.0	414	3 AAZ33123	Aaz33123 Wasabia j
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41	217	74.6	1973	3 AAC46924	Aac46924 Arabidops
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43	211	72.5	284	2 AAQ70129	AaQ70129 Antimicro
44	201	69.1	306	2 AAT94580	Aat94580 Cloned 3,
45	160	55.0	658	5 AAAS4389	Aaas4389 Plant def

ALIGNMENTS

RESULT 1	AAQ38652	AAQ38652 standard; DNA; 261 BP.
ID	AAQ38652	
XX	XX	
AC	AAQ38652;	
XX	XX	
DT	25-MAR-2003 (revised)	
DT	07-JUL-1993 (first entry)	
XX	XX	
DE	Rs-APP2 CDNA.	
XX	XX	
KW	Raphanus sativus; Brassica; Arabidopsis; Cnicus; Lathyrus; Clitoria;	
KW	fungicide; bactericide; antibiotic; antifungal; gram positive;	
KW	plant disease resistance; low toxicity.	
XX	XX	
OS	Raphanus sativus.	
XX	XX	
FH	Key	Location/Qualifiers
CDS	16..256	
FT	/*tag= a	
XX	XX	
PN	WO9305153-A1.	
XX	XX	
PD	18-MAR-1993.	
XX	XX	
FF	27-AUG-1992;	92WO-GB001570.
XX	XX	
PR	29-AUG-1991;	91GB-00018523.
PR	13-FEB-1992;	92GB-00003038.
PR	25-JUN-1992;	92GB-00013526.
XX	XX	
PA	(ICIL ) IMPERIAL CHEM IND PLC.	



XX PI Broekaert WF, Cammue BPA, Osborn RW, Rees SB, Terras FRG;  
 XX PI Vanderleyden J;  
 XX WPI; 1993-100978/12.  
 XX Biotic proteins isolated from seeds of plants - e.g. brassica or  
 PT dahlia, useful for increasing plants' resistance to fungal and bacterial  
 PT diseases.  
 XX Example 21; Fig 35; 110pp; English.  
 XX This cDNA represents the sequence of Rs-APP2 from *Raphanus sativus*. PCR  
 CC primer AAQ38640 was used together with AAQ38641 to generate a probe for  
 CC screening a *Raphanus sativus* seed cDNA library. This primer corresponds  
 CC to amino acids 2 to 7 of Rs-APP1 and has a sense orientation. The 144bp  
 CC product was partially re-amplified using AAQ38642 and AAQ38641 to give a  
 CC 123bp product, which was further reamplified with the same primers and  
 CC digoxigenin-11-dUTP instead of dTTP to give a digoxigenin labeled PCR  
 CC product. This was used to screen a lambda ZAPII cDNA library by in situ  
 CC plaque hybridisation. Positive plaques were purified and subjected to two  
 CC additional screening rounds with the same probe. Inserts were excised in  
 CC vivo into the pBluescript phagemid form with the aid of helper phage  
 CC R409. Inserts from 22 positive clones were excised by EcoRI digestion and  
 CC their size compared by agarose gel electrophoresis. Four clones had  
 CC insert sizes of approx. 400bp the others between 250-300bp. The inserts  
 CC of the 4 largest clones were then sequenced and found to differ only in  
 CC the length of their 5' and 3' UTR's. The longest sequence was identified  
 CC as Rs-APP1 (AAQ38650). Rs-APP2 was seen to differ by only 2 amino acids  
 CC from Rs-APP1, so the Rs-APP1 cDNA was transformed to the Rs-APP2  
 CC nucleotide sequence by PCR assisted site directed mutagenesis. (Updated  
 CC on 25-MAR-2003 to correct PN field.)  
 XX SQ Sequence 261 BP; 67 A; 55 C; 59 G; 80 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,238-25 Length: 261  
 Score: 291.00 Matches: 47  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0  
 SEQ9-X-AT-5-9-16-39 (1-51) x AAQ38652 (1-261)  
 QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAsnAla 20  
 Db 103 CAGAAAGTTGTGCCAAGGCGCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 162  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 Db 163 TCGAAGATCATGTGCATTAGACTTTGAAAGACACACATGATCTTGCACACTATGCTTTC 222  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 Db 223 CCAGCTCACAGTGTATCTGCTACTTCTTCTTGT 255  
 RESULT 2  
 AAQ70130  
 ID AAQ70130 standard; cDNA; 288 BP.  
 XX AC AAQ70130;  
 XX DT 25-MAR-2003 (revised)  
 XX DT 14-FEB-1995 (first entry)  
 DE Antimicrobial Rs-APP2.  
 XX Antimicrobial; Rs-APP2; symbiosis; disease-resistance; fungus-resistance;  
 KW *Clavibacter xyli* subsp. *cynodontis*; Cxc; crop improvement; endophyte;  
 KW PCR; polymerase chain reaction; mutagenesis; ss.  
 XX *Raphanus sativus*.  
 OS

XX WO9416076-A1.  
 XX 21-JUL-1994.  
 XX 05-JAN-1994; 94WO-GB000012.  
 XX 08-JAN-1993; 93GB-00000281.  
 XX (ZENE) ZENECA LTD.  
 XX Dubock AC, Powell KA, Rees SB;  
 XX WPI; 1994-249223/30.  
 DR P-PSDB; AAR57327.  
 DR Antimicrobial protein producing endo-symbiotic microorganisms - is  
 PT produced by combining nucleic acids encoding the protein with an  
 PT endophyte, useful for protecting plant hosts from esp. fungal disease.  
 XX Disclosure; Page 33; 39pp; English.  
 PS Plant-derived antimicrobial proteins are expressed in endosymbiotic  
 CC *Clavibacter xyli* subsp. *cynodontis* (Cxc). Plants or seeds treated with  
 CC recombinant Cxc are protected against fungal disease. A suitable  
 CC antimicrobial protein is Rs-APP1 from *R. sativus*. The full-length cDNA  
 CC sequence of PCR assisted site-directed mutagenesis of Rs-APP2 is given in  
 CC AAQ70130 and the deduced amino acid sequence in AAR57327. (Updated on 25-  
 CC MAR-2003 to correct PN field.)  
 XX SQ Sequence 288 BP; 70 A; 66 C; 69 G; 83 T; 0 U; 0 Other;  
 SQ  
 Alignment Scores:  
 Pred. No.: 1,48-25 Length: 288  
 Score: 291.00 Matches: 47  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 2 Gaps: 0  
 SEQ9-X-AT-5-9-16-39 (1-51) x AAQ70130 (1-288)  
 QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAsnAla 20  
 Db 130 CAGAAGTTGTGCCAAGGCGCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA 189  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 Db 190 TCGAAGATCATGTGCATTAGACTTTGAAAGACACACATGATCTTGCACACTATGCTTTC 249  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 Db 250 CCAGCTCACAGTGTATCTGCTACTTCTTCTTGT 282  
 RESULT 3  
 AAZ99332  
 ID AAZ99332 standard; DNA; 434 BP.  
 XX AC AAZ99332;  
 XX XX 03-JUL-2000 (first entry)  
 XX DE DNA encoding a fusion protein of DnaMPL and RsAPP2.  
 XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KW protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.  
 XX Synthetic.  
 OS *Dahlia merckii*.  
 OS Unidentified.  
 XX Key Location/Qualifiers  
 FT CDS 3..425

FT /\*tag= a  
 FT /product= "fusion protein of DmAMP1 and RsAPP2"  
 PN WO200011175-A1.

XX 02-MAR-2000.

PF 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1998; 98GB-00018001.

PR 04-DEC-1998; 98GB-00026753.

XX (ZENE ) ZENECA LTD.

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

DR P-PSDB; AAY84065.

XX Improving expression of polyproteins in plants involves coexpression of  
 two or more proteins in plants within a single transcription unit.

PS Disclosure; Fig 27; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the  
 mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker  
 propeptide of the invention. The specification describes methods for  
 improving expression levels of one or more proteins in a transgenic  
 plant. The method comprises inserting a DNA sequence having a promoter  
 region operably linked to two or more protein encoding regions separated  
 by a DNA sequence coding for a linker propeptide and a terminator region.  
 The method is used to produce proteins in plants. The linker propeptide  
 comprising a cleavage site, whereby the expressed polypeptide is post-  
 translationally processed into the component protein molecules. The  
 propeptide sequence is rich in amino acids A, V, S and T and contains  
 dipeptidic sequences consisting of either two acidic, two basic or one  
 acidic and one basic residue as a cleavable linker sequence

XX Sequence 434 BP; 108 A; 101 C; 117 G; 108 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,426-25 Length: 434  
 Score: 291.00 Matches: 47  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99332 (1-434)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAla 20  
 DB 270 CAGAAAGTTGTGCCAAGGCCAAGTCGTACATGTCAGAGTCTGTGGAAACATACGCA 329  
 QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 DB 330 TGCAGAATCATGTCGATTTAGACTTTGAGAAACACGACATGGATCTTGCAACTATCGTTTC 389

QY 41 ProAlaHisLysCysIleCysTyr:PheProCys 51

DB 390 CCAGCTCACAGTGTATCTGCTACTTCTTGT 422

RESULT 4

ID AAZ99331

XX AAZ99331 standard; DNA; 437 BP.

XX AAZ99331;

XX 03-JUL-2000 (first entry)

XX DNA encoding a fusion protein of DmAMP1 and RsAPP2.

XX

KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KW protein expression; plant defensin; RsAPP2; antifungal protein; AFP2; ss.  
 OS Synthetic.  
 OS Dahlia merckii.  
 OS Unidentified.

XX Key Location/Qualifiers  
 FT 3..428  
 FT CDS /\*tag= a  
 FT /product= "fusion protein of DmAMP1 and RsAPP2"

XX WO200011175-A1.

XX 02-MAR-2000.

PF 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1998; 98GB-00018001.

PR 04-DEC-1998; 98GB-00026753.

XX (ZENE ) ZENECA LTD.

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

DR P-PSDB; AAY84064.

XX Improving expression of polyproteins in plants involves coexpression of  
 two or more proteins in plants within a single transcription unit.

PS Disclosure; Fig 26; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the  
 mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 (AMP) 1 and the antifungal protein 2 (APP2), linked by a linker  
 propeptide of the invention. The specification describes methods for  
 improving expression levels of one or more proteins in a transgenic  
 plant. The method comprises inserting a DNA sequence having a promoter  
 region operably linked to two or more protein encoding regions separated  
 by a DNA sequence coding for a linker propeptide and a terminator region.  
 The method is used to produce proteins in plants. The linker propeptide  
 comprising a cleavage site, whereby the expressed polypeptide is post-  
 translationally processed into the component protein molecules. The  
 propeptide sequence is rich in amino acids A, V, S and T and contains  
 dipeptidic sequences consisting of either two acidic, two basic or one  
 acidic and one basic residue as a cleavable linker sequence

XX Sequence 437 BP; 109 A; 102 C; 118 G; 108 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,44e-25 Length: 437  
 Score: 291.00 Matches: 47  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99331 (1-437)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAla 20  
 DB 273 CAGAAAGTTGTGCCAAGGCCAAGTCGTACATGTCAGAGTCTGTGGAAACATACGCA 332

QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 DB 333 TGCAGAATCATGTCGATTTAGACTTTGAGAAACACGACATGGATCTTGCAACTATCGTTTC 392

QY 41 ProAlaHisLysCysIleCysTyr:PheProCys 51

DB 393 CCAGCTCACAGTGTATCTGCTACTTCTTGT 425

RESULT 5

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AAZ99330
ID AAZ99330 standard; DNA; 443 BP.
AC AAZ99330;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.
XX
KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
XX
OS Synthetic.
OS Dahlia merckii.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 3..434
FT FT /*tag= a
FT FT /product= "fusion protein of DmAMP1 and RsAFP2"
XX
PN WO200011175-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-GB002716.
XX
PR 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX
PA (ZONE ) ZENECA LTD.
XX
PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX
DR WPI; 2000-246564/21.
DR P-PSDB; AAY84063.
XX
PT Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
PS Disclosure; Fig 25; 151pp; English.
XX
CC The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site, whereby the expressed polypeptide is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 443 BP; 111 A; 102 C; 121 G; 109 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,49e-25 Length: 443
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99330 (1-443)

QY 1 GlnlystleuCyS**ArgProSer***ThrTrpSerGlyValCyS***AsnAsnAla 20
DB 279 CAGAGTTGTGCCAAGGCCCAAGTCGTACATGCTCAGGAGTCTGTGGACACATACCGCA 338

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QY 21 CyslyshenGlnCySilleArygLeuGluValAalaAroHisGlySerCySAsnTy***Phe 40
DB 339 TGCAGATCATGTCATAGCATTTGAGAAAGCAGACATGGAATCTTGCACACTACGTTTC 398
QY 41 ProAlahisLySylleCySlyTyPheProCyS 51
DB 399 CCAGCTCAAGTGTATCTGCTACTTTCCTTGT 431

RESULT 6
AAZ99329
ID AAZ99329 standard; DNA; 446 BP.
XX
AC AAZ99329;
XX
DT 03-JUL-2000 (first entry)
XX
DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.
XX
KW Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
XX
OS Synthetic.
OS Dahlia merckii.
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 3..437
FT FT /*tag= a
FT FT /product= "fusion protein of DmAMP1 and RsAFP2"
XX
PN WO200011175-A1.
XX
PD 02-MAR-2000.
XX
PF 17-AUG-1999; 99WO-GB002716.
XX
PR 18-AUG-1998; 98GB-00018001.
PR 04-DEC-1998; 98GB-00026753.
XX
PA (ZONE ) ZENECA LTD.
XX
PI Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX
DR WPI; 2000-246564/21.
DR P-PSDB; AAY84062.
XX
PT Improving expression of polyproteins in plants involves coexpression of
PT two or more proteins in plants within a single transcription unit.
XX
PS Disclosure; Fig 24; 151pp; English.
XX
CC The present sequence encodes a protein of the invention, comprising the
CC mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
CC propeptide of the invention. The specification describes methods for
CC improving expression levels of one or more proteins in a transgenic
CC plant. The method comprises inserting a DNA sequence having a promoter
CC region operably linked to two or more protein encoding regions separated
CC by a DNA sequence coding for a linker propeptide and a terminator region.
CC The method is used to produce proteins in plants. The linker propeptide
CC comprising a cleavage site, whereby the expressed polypeptide is post-
CC translationally processed into the component protein molecules. The
CC propeptide sequence is rich in amino acids A, V, S and T and contains
CC dipeptidic sequences consisting of either two acidic, two basic or one
CC acidic and one basic residue as a cleavable linker sequence
XX
SQ Sequence 446 BP; 111 A; 102 C; 123 G; 110 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,51e-25 Length: 446
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0

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Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99329 (1-446)			
Qy	1	GlnLysLeuCys***ArgProSer***ThrTyrSerGlyValCys***AsnAsnAla	20
Db	282	CAGAAGTTGTGCCAAGCCCAAGTCGTACATGTCAGAGTCGTGGAAACATAACGCA	341
Qy	21	CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe	40
Db	342	TGCAAGATCAGTCATAGACTTGAGAAAGCAGACATGATCTTGCAACTATCGTTTC	401
Qy	41	ProLahisLysCysIleCysTyrPheProCys	51
Db	402	CCAGCTCACAGTGTATCTGCTACTTTCCTGT	434
RESULT 7			
AAAS3190			
ID	AAAS3190	standard; DNA; 449 BP.	
XX	AAAS3190;		
DT	06-OCT-2000	(first entry)	
DE	Raphanus sativus antibacterial protein radishin encoding DNA SEQ ID NO:1.		
XX	Raphanus sativus; antibacterial; plant; resistance; paddy; radishin;		
XX	pathogenic microbe; radish; rice blast disease; ds.		
OS	Raphanus sativus.		
PN	JP2000116379-A.		
PD	25-APR-2000.		
XX	09-OCT-1998;	98JP-00288472.	
XX	09-OCT-1998;	98JP-00288472.	
XX	(TOYA-) TOYAMA KEN.		
XX	WPI; 2000-389821/34.		
DR	P-PSDB; AAY91117.		
XX	Isolated DNA from Raphanus sativus used to transform a microbe and a		
PT	plant to produce an antibacterial protein used to increase resistance of		
PT	rice paddy against pathogenic microbes.		
XX	Claim 1; Page 4; 7pp; Japanese.		
XX	The present sequence encodes an antibacterial protein, designated		
CC	radishin, isolated from Raphanus sativus (radish). A phase or plasmid		
CC	comprising radishin can be used for increasing resistance of paddy and		
CC	rice blast disease against pathogenic microbes		
XX	Sequence 449 BP; 126 A; 78 C; 94 G; 151 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	2,53e-25	Length:	449
Score:	291.00	Matches:	47
Percent Similarity:	100.00%	Conservative:	4
Best Local Similarity:	92.16%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0
SEQ9-X-AT-5-9-16-39 (1-51) x AAAS3190 (1-449)			
Qy	1	GlnLysLeuCys***ArgProSer***ThrTyrSerGlyValCys***AsnAsnAla	20
Db	128	CAGAAGTTGTGTCAGAGCCCAAGTCGTACATGTCAGAGTCGTGGAAATATACGCA	187
Qy	21	CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe	40
Db	188	TGCAAGATCAGTCATAGACTTGAGAAAGCAGACATGATCTTGCAACTATCGTTTC	247
Qy	41	ProLahisLysCysIleCysTyrPheProCys	51
Db	248	CCAGCTCACAGTGTATCTGCTACTTTCCTGT	280
RESULT 8			
AAZ99333			
ID	AAZ99333	standard; DNA; 485 BP.	
XX	AAZ99333;		
DT	03-JUL-2000	(first entry)	
DE	DNA encoding a fusion protein of DmAMP1 and RsAFP2.		
XX	Antimicrobial protein; AMP1; transgenic plant; linker propeptide;		
XX	protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.		
OS	Synthetic.		
OS	Dahlia merckii.		
OS	Unidentified.		
XX	Key	Location/Qualifiers	
FT	CDS	3..476	
FT	FT	/*tag= a	
FT	FT	/product= "fusion protein of DmAMP1 and RsAFP2"	
XX	WO200011175-A1.		
XX	02-MAR-2000.		
XX	17-AUG-1999;	99WO-GB002716.	
XX	18-AUG-1998;	98GB-00018001.	
PR	04-DEC-1998;	98GB-00025753.	
XX	(ZENE ) ZENECA LTD.		
XX	Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;		
XX	WPI; 2000-246564/21.		
DR	P-PSDB; AAY84066.		
XX	Improving expression of polyproteins in plants involves coexpression of		
PT	two or more proteins in plants within a single transcription unit.		
XX	Disclosure; Fig 28; 151pp; English.		
XX	The present sequence encodes a protein of the invention, comprising the		
CC	mature proteins of the plant defensin, the Dahlia antimicrobial protein		
CC	(AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker		
CC	propeptide of the invention. The specification describes methods for		
CC	improving expression levels of one or more proteins in a transgenic		
CC	plant. The method comprises inserting a DNA sequence having a promoter		
CC	region operably linked to two or more protein encoding regions separated		
CC	by a DNA sequence coding for a linker propeptide and a terminator region.		
CC	The method is used to produce proteins in plants. The linker propeptide		
CC	comprising a cleavage site, whereby the expressed polypeptide is post-		
CC	translationally processed into the component protein molecules. The		
CC	propeptide sequence is rich in amino acids A, V, S and T and contains		
CC	dipeptidic sequences consisting of either two acidic, two basic or one		
CC	acidic and one basic residue as a cleavable linker sequence		
XX	Sequence 485 BP; 124 A; 107 C; 128 G; 126 T; 0 U; 0 Other;		
Alignment Scores:			
Pred. No.:	2,81e-25	Length:	485
Score:	291.00	Matches:	47
Percent Similarity:	100.00%	Conservative:	4
Best Local Similarity:	92.16%	Mismatches:	0
Query Match:	100.00%	Indels:	0

DB:	3	Gaps:	0
SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99333 (1-485)			
QY	1	GlnLysLeuCyse**ArgProSer**ThrTrpSerGlyValCys***AsnAsnAsnAla 20	
Db	321	CAGAAGTTGTGCGCAAGGCCAAGTCGTACATGGTCAGGAGTCGTGTGGAAACAATAACGCA 380	
QY	21	CysLysAsnGlnCysIleArgLeuLysAlaArgHisGlySerCysAsnTyr***Phe 40	
Db	381	TGCAGAAGTCAGTCATTAGACTTGAGAAAGCAGCATGTCCTCAACTATCGTTTC 440	
QY	41	ProAlaHisLysCysIleCysTyrPheProCys 51	
Db	441	CCAGCTCACAAGTGTATCTGCTACTTTCCTTGT 473	
RESULT 9			
AAZ99335			
ID	AAZ99335	standard; DNA; 485 BP.	
XX	AAZ99335;		
XX	03-JUL-2000	(first entry)	
DE	XX	DNA encoding a fusion protein of DmAMP1 and RsAPP2.	
XX	XX	Antimicrobial protein; AMP1; transgenic plant; linker propeptide;	
KW	XX	protein expression; plant defensin; RsAPP2; antifungal protein; APP2; ss.	
OS	XX	Synthetic.	
OS	XX	Dahlia merckii.	
OS	XX	Unidentified.	
XX	Key	Location/Qualifiers	
FT	CDS	3..476	
FT	FT	/*tag= a	
FT	FT	/product= "fusion protein of DmAMP1 and RsAPP2"	
XX	XX	WO200011175-A1.	
XX	XX	02-MAR-2000.	
XX	XX	17-AUG-1999; 99WO-GB002716.	
XX	XX	18-DEC-1998; 98GB-00018001.	
PR	XX	04-DEC-1998; 98GB-00026753.	
XX	XX	(ZENE ) ZENECA LTD.	
XX	XX	Broekaert WF, Francois IEJA, De Bolle MFC, Evans LJ, Ray JA;	
XX	XX	WPI; 2000-246564/21.	
DR	XX	P-PSDB; AAY84068.	
XX	XX	Improving expression of polyproteins in plants involves coexpression of	
PT	XX	two or more proteins in plants within a single transcription unit.	
XX	XX	Disclosure; Fig 30; 151pp; English.	
PS	XX	The present sequence encodes a protein of the invention, comprising the	
CC	XX	mature proteins of the plant defensins, the Dahlia antimicrobial protein	
CC	XX	(AMP) 1 and the antifungal protein 2 (RsAPP2), linked by a linker	
CC	XX	propeptide of the invention. The specification describes methods for	
CC	XX	improving expression levels of one or more proteins in a transgenic	
CC	XX	plant. The method comprises inserting a DNA sequence having a promoter	
CC	XX	region operably linked to two or more protein encoding regions separated	
CC	XX	by a DNA sequence coding for a linker propeptide and a terminator region.	
CC	XX	The method is used to produce proteins in plants. The linker propeptide	
CC	XX	comprising a cleavage site, whereby the expressed polyprotein is post-	
CC	XX	translationally processed into the component protein molecules. The	
CC	XX	propeptide sequence is rich in amino acids A, V, S and T and contains	
CC	XX	dipeptidic sequences consisting of either two acidic, two basic or one	
CC	XX	acidic and one basic residue as a cleavable linker sequence	

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XX      Sequence 485 BP; 139 A, 104 C; 128 G; 114 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.:          2.8ie-25          Length:          485
Score:              291.00           Matches:         47
Percent Similarity: 100.00%           Conservative:    4
Best Local Similarity: 92.16%           Mismatches:     0
Query Match:        100.00%           Indels:         0
DB#:                3                 Gaps:           0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99335 (1-485)

Qy      1 GlrLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AenAsnAenAla 20
Db      321 CAGAAGTTGTGCCAAAGCCCAAGTCGTACATCGTTCAGGAGCTCTGTGGAAAACAATAACGCA 380
Qy      21 CysLysAenGlnCysIleArxLeuGluLyAlaAargHisGlySerCysAenTyR***Phe 40
Db      381 TCAGATCATCGATTGACTTAGATCTTGAGAAAGCACGACATGGAICTTGCAACTATCGTTTC 440
Qy      41 ProAlaHisLysCysIleCyseTy:PheProCys 51
Db      441 CCAGCTCACAAGTGATCTGCTACTTTCCTTGT 473

RESULT 10
AAZ99337
ID   AAZ99337 standard; DNA; 485 BP.
AC
AC   AAZ99337;
XX
XX   03-JUL-2000 (first entry)
XX
XX   DNA encoding a fusion protein of DmAMP1 and RsAFP2.
XX
XX   Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
KW   protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; s.
XX
XX   Synthetic.
OS   Dahlia merckii.
OS   Unidentified.
XX
XX   Key Location/Qualifiers
FH   3..476
FT   CDS
FT   /tag= a
FT   /product= "fusion protein of DmAMP1 and RsAFP2"
XX
XX   WO200011175-A1.
XX
XX   02-MAR-2000.
XX
XX   17-AUG-1999; 99WO-GB002716.
XX
XX   18-AUG-1998; 98GB-00018001.
PR   04-DEC-1998; 98GB-00026753.
XX
XX   (ZONE ) ZENECA LTD.
XX
XX   Broekaert WF, Francois IEUA, De Bolle MFC, Evans IJ, Ray JA;
PI
XX   WPI; 2000-246564/21.
DR   P-FSDB; AAY84070.
DR
XX
Improving expression of polyproteins in plants involves coexpression of
two or more proteins in plants within a single transcription unit.
PS   Disclosure; Fig 32; 151pp; English.
XX
XX   The present sequence encodes a protein of the invention, comprising the
CC   mature proteins of the plant defensins, the Dahlia antimicrobial protein
CC   (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker
CC   propeptide of the invention. The specification describes methods for
CC   improving expression levels of one or more proteins in a transgenic

```

CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX  
 SQ Sequence 485 BP; 129 A; 106 C; 131 G; 119 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 2,81e-25 Length: 485  
 Score: 291.00 Matches: 47  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99337 (1-485)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTpsrGlyValCys\*\*\*AsnAsnAla 20  
 DB 321 CAGAGTTGTGCCAAGCCCAAGTCGTACATGTCAGAGTCTGTGGAAACATACGCA 380  
 QY 21 CysLysAsnGlnCysIleArgLeuGlulysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 DB 381 TGCAGAAATCAGTCGATTCAGTTCGAGAACGACGACATGATCTTGCACATCTCTGTC 440

QY 41 ProLahisLysCysIleCysTyrPheProCys 51  
 DB 441 CCAGTCAACAGTGTATCTGCTACTTCTCTGT 473

RESULT 11

AAZ99338  
 ID AAZ99338 standard; DNA; 488 BP.

AC AAZ99338;

DT 03-JUL-2000 (first entry)

DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.

XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.

XX Synthetic.

OS Dahlia merckii.

OS Unidentified.

XX Key Location/Qualifiers

FT CDS 3..479

FT /\*tag= a  
 FT /product= "fusion protein of DmAMP1 and RsAFP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

XX 18-AUG-1998; 98GB-00018001.

PR 04-DEC-1998; 98GB-00026753.

XX (ZENE) ZENECA LTD.

XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;

XX WPI; 2000-246564/21.

DR P-PSDB; AA84071.

XX Improving expression of polyproteins in plants involves coexpression of

PT

PT two or more proteins in plants within a single transcription unit.  
 XX Disclosure; Fig 33; 151pp; English.

XX The present sequence encodes a protein of the invention, comprising the  
 CC mature proteins of the plant defensins, the Dahlia antimicrobial protein  
 CC (AMP) 1 and the antifungal protein 2 (RsAFP2), linked by a linker  
 CC propeptide of the invention. The specification describes methods for  
 CC improving expression levels of one or more proteins in a transgenic  
 CC plant. The method comprises inserting a DNA sequence having a promoter  
 CC region operably linked to two or more protein encoding regions separated  
 CC by a DNA sequence coding for a linker propeptide and a terminator region.  
 CC The method is used to produce proteins in plants. The linker propeptide  
 CC comprising a cleavage site, whereby the expressed polypeptide is post-  
 CC translationally processed into the component protein molecules. The  
 CC propeptide sequence is rich in amino acids A, V, S and T and contains  
 CC dipeptidic sequences consisting of either two acidic, two basic or one  
 CC acidic and one basic residue as a cleavable linker sequence  
 XX  
 SQ Sequence 488 BP; 117 A; 116 C; 131 G; 124 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,83e-25 Length: 488  
 Score: 291.00 Matches: 47  
 Percent Similarity: 100.00% Conservative: 4  
 Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AAZ99338 (1-488)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTpsrGlyValCys\*\*\*AsnAsnAla 20  
 DB 324 CAGAGTTGTGCCAAGCCCAAGTCGTACATGTCAGAGTCTGTGGAAACATACGCA 383  
 QY 21 CysLysAsnGlnCysIleArgLeuGlulysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 DB 384 TGCAGAAATCAGTCGATTCAGTTCGAGAACGACGACATGATCTTGCACATCTCTGTC 443  
 QY 41 ProLahisLysCysIleCysTyrPheProCys 51  
 DB 444 CCAGTCAACAGTGTATCTGCTACTTCTCTGT 476

RESULT 12

AAZ99324  
 ID AAZ99324 standard; DNA; 522 BP.

AC AAZ99324;

DT 03-JUL-2000 (first entry)

DE DNA encoding a fusion protein of DmAMP1 and RsAFP2.

XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;  
 KW protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.

XX Synthetic.

OS Dahlia merckii.

OS Unidentified.

XX Key Location/Qualifiers

FT misc\_feature 160..309

FT /\*tag= a  
 FT /note= "encodes DmAMP1"

FT misc\_feature 358..510

FT /\*tag= b  
 FT /note= "encodes RsAFP2"

XX WO200011175-A1.

XX 02-MAR-2000.

XX 17-AUG-1999; 99WO-GB002716.

XX



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PH Key      Location/Qualifiers
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FT          /*tag= a
FT misc_feature 162..309
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FT          /note= "encodes DmAMP1"
FT misc_feature 372..519
FT          /*tag= c
FT          /note= "encodes RsAFP2"
XX WO200011175-A1.
XX
XX 02-MAR-2000.
XX
XX 17-AUG-1999; 99WO-GB002716.
XX
XX 18-AUG-1998; 98GB-00018001.
XX 04-DEC-1998; 98GB-00026753.
XX (ZENE ) ZENECA LTD.
XX
XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI; 2000-246564/21.
XX P-PSDB; AAY84060.
XX
XX Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX
XX Example 2; Fig 12; 151pp; English.
XX
XX The present sequence encodes a protein of the invention, comprising the
XX mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
XX propeptide of the invention. The specification describes methods for
XX improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polyprotein is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
XX SQ Sequence 534 BP; 154 A; 120 C; 125 G; 135 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.19e-25 Length: 534
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AA299327 (1-534)
Qy 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 370 CAGAAAGTGTGCCAAGCCCAAGTGGACATGGTCAGGAGTCTGTGTGGAACATAACGCA 429
Qy 21 CysLysAsnGlnCysIleAArgLeuGluLeuAlaArgHisGlySerCysAsnTyr***Phe 40
Db 430 TGCAAGATCAGTCAGTCATTAGACTTGAGAAAGCAGACATGATCTTGCACTATGCTTC 489
Qy 41 ProLHisLysCysIleCysTyrPheProCys 51
Db 490 CCAGCTCACAGTGTATCTGCTACTTTCCTGT 522

RESULT 15
AAZ99325
ID AA299325 standard; DNA; 534 BP.

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XX AA299325;
XX 03-JUL-2000 (first entry)
XX
XX DNA encoding a fusion protein of DmAMP1 and RsAFP2.
XX
XX Antimicrobial protein; AMP1; transgenic plant; linker propeptide;
XX protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
XX
XX Synthetic.
XX Dahlia merckii.
XX Unidentified.
XX
XX Key      Location/Qualifiers
XX CDS      76..522
XX          /*tag= a
XX misc_feature 160..309
XX          /*tag= b
XX          /note= "encodes DmAMP1"
XX misc_feature 370..538
XX          /*tag= c
XX          /note= "encodes RsAFP2"
XX
XX WO200011175-A1.
XX
XX 02-MAR-2000.
XX
XX 17-AUG-1999; 99WO-GB002716.
XX
XX 18-AUG-1998; 98GB-00018001.
XX 04-DEC-1998; 98GB-00026753.
XX (ZENE ) ZENECA LTD.
XX
XX Broekaert WF, Francois IEJA, De Bolle MFC, Evans IJ, Ray JA;
XX WPI; 2000-246564/21.
XX P-PSDB; AAY84058.
XX
XX Improving expression of polyproteins in plants involves coexpression of
XX two or more proteins in plants within a single transcription unit.
XX
XX Example 2; Fig 9; 151pp; English.
XX
XX The present sequence encodes a protein of the invention, comprising the
XX mature proteins of the plant defensins, the Dahlia antimicrobial protein
XX (AMP) 1 and the antifungal protein 2 (AFP2), linked by a linker
XX propeptide of the invention. The specification describes methods for
XX improving expression levels of one or more proteins in a transgenic
XX plant. The method comprises inserting a DNA sequence having a promoter
XX region operably linked to two or more protein encoding regions separated
XX by a DNA sequence coding for a linker propeptide and a terminator region.
XX The method is used to produce proteins in plants. The linker propeptide
XX comprising a cleavage site, whereby the expressed polyprotein is post-
XX translationally processed into the component protein molecules. The
XX propeptide sequence is rich in amino acids A, V, S and T and contains
XX dipeptidic sequences consisting of either two acidic, two basic or one
XX acidic and one basic residue as a cleavable linker sequence
XX
XX SQ Sequence 534 BP; 164 A; 118 C; 122 G; 130 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.19e-25 Length: 534
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x AA299325 (1-534)
Qy 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20

```



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Db 370 CAGAACTTGTGCGCAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACAATACCCA 429
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 430 TCGAAGAATCAGTGCATTAGACTTGAGAAAGCAGACATGGATCTTGCACACTATGTCCTTC 489
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 490 CCAGCTCACAAAGTGTATCTGCTACTTTCCTTGT 522
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GenCore version 5.1.6  
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Run on: March 24, 2004, 05:44:19 ; Search time 82 seconds  
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345.152 Million cell updates/sec

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Perfect score: 291  
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#### SUMMARIES

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2	291	100.0	285	3	US-09-103-489-17
3	291	100.0	285	4	US-09-829-381D-17
4	291	100.0	288	1	US-08-377-687-58
5	291	100.0	288	3	US-08-777-192-58
6	291	100.0	288	3	US-08-971-982-58
7	286	98.3	285	1	US-08-627-706-16
8	286	98.3	285	3	US-09-103-489-16
9	286	98.3	285	4	US-09-829-381D-16
10	286	98.3	414	1	US-08-377-687-48
11	286	98.3	414	1	US-08-777-192-48
12	286	98.3	414	3	US-08-971-982-48

13	286	98.3	414	4	US-09-077-951-19	Sequence 19, Appl
14	286	98.3	414	4	US-09-077-948A-45	Sequence 45, Appl
15	289	92.4	308	1	US-08-627-706-5	Sequence 5, Appl
16	269	92.4	308	3	US-09-103-489-5	Sequence 5, Appl
17	269	92.4	308	4	US-09-829-381D-5	Sequence 5, Appl
18	260	89.3	270	1	US-08-627-706-14	Sequence 14, Appl
19	260	89.3	270	3	US-09-103-489-14	Sequence 14, Appl
20	260	89.3	270	4	US-09-829-381D-14	Sequence 14, Appl
21	260	89.3	286	1	US-08-627-706-12	Sequence 12, Appl
22	260	89.3	286	3	US-09-103-489-12	Sequence 12, Appl
23	260	89.3	286	4	US-08-627-706-9	Sequence 9, Appl
24	258	88.7	500	1	US-09-103-489-9	Sequence 9, Appl
25	258	88.7	500	3	US-09-829-381D-9	Sequence 9, Appl
26	258	88.7	500	4	US-08-377-687-31	Sequence 31, Appl
27	211	72.5	284	1	US-08-777-192-50	Sequence 50, Appl
28	211	72.5	284	3	US-08-971-982-50	Sequence 50, Appl
29	211	72.5	306	1	US-08-627-706-8	Sequence 8, Appl
30	201	69.1	306	3	US-09-103-489-8	Sequence 8, Appl
31	201	69.1	306	4	US-09-829-381D-8	Sequence 8, Appl
32	201	69.1	306	1	US-08-377-687-31	Sequence 31, Appl
33	150	51.5	150	1	US-08-777-192-31	Sequence 31, Appl
34	150	51.5	150	3	US-08-971-982-31	Sequence 31, Appl
35	150	51.5	150	4	US-08-377-687-34	Sequence 34, Appl
36	147	50.5	150	1	US-08-777-192-34	Sequence 34, Appl
37	147	50.5	150	3	US-08-971-982-34	Sequence 34, Appl
38	147	50.5	150	4	US-08-377-687-33	Sequence 33, Appl
39	145	49.8	150	1	US-08-777-192-33	Sequence 33, Appl
40	145	49.8	150	3	US-08-971-982-33	Sequence 33, Appl
41	145	49.8	150	4	US-09-589-733C-6	Sequence 6, Appl
42	142	48.8	147	1	US-08-377-687-36	Sequence 36, Appl
43	136.5	46.9	147	1	US-08-777-192-36	Sequence 36, Appl
44	136.5	46.9	147	3	US-08-971-982-36	Sequence 36, Appl
45	136.5	46.9	147	3	US-08-971-982-36	Sequence 36, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-627-706-17  
; Sequence 17, Application US/08627706  
; Patent No. 5773696  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yonnie S.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, B84F  
; STREET: 700 Chesterfield Village Parkway No. 5773696th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,706  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 17:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 285 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: other nucleic acid
;   DESCRIPTION: /desc = "synthetic DNA"
US-08-627-706-17

Alignment Scores:
Pred. No.: 4,86e-28 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-627-706-17 (1-285)
QY 1 GlnLysLeuCys***ArgProSer***ThrTTPSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGCAGAACCAATGCATCAGACTCGAGAAGGCACGGCATGGATCTTGCAACTACGCTTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 2
US-09-103-489-17
; Sequence 17, Application US/09103489
; Patent No. 6215048
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/103,489
; FILING DATE: 24-JUN-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21 (10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314) 537-6224
; TELEFAX: (314) 537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 285 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   MOLECULE TYPE: other nucleic acid

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; DESCRIPTION: /desc = "synthetic DNA"
US-09-103-489-17

Alignment Scores:
Pred. No.: 4,86e-28 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-103-489-17 (1-285)
QY 1 GlnLysLeuCys***ArgProSer***ThrTTPSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGCAGAACCAATGCATCAGACTCGAGAAGGCACGGCATGGATCTTGCAACTACGCTTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 3
US-09-829-381D-17
; Sequence 17, Application US/09829381D
; Patent No. 6653280
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong
; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yennie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control
; REFERENCE/DOCKET NUMBER: 38-21 (10700) C
; CURRENT APPLICATION NUMBER: US/09/829,381D
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/103,489
; FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-829-381D-17

Alignment Scores:
Pred. No.: 4,86e-28 Length: 285
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381D-17 (1-285)
QY 1 GlnLysLeuCys***ArgProSer***ThrTTPSerGlyValCys***AsnAsnAsnAla 20
Db 118 CAAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGCAGAACCAATGCATCAGACTCGAGAAGGCACGGCATGGATCTTGCAACTACGCTTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTTCATGC 270

```

## RESULT 4

US-08-377-687-58  
; Sequence 58, Application US/08377687  
; Patent No. 5538525  
; GENERAL INFORMATION:  
; APPLICANT: BROEKART, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/377,687  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 43..282  
US-08-377-687-58

Alignment Scores:  
Pred. No.: 4,93e-28 Length: 288  
Score: 291.00 Matches: 47  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-377-687-58 (1-288)

QY	1	GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAsnAla	20
DB	130	CAGAAGTTGTGCCAAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA	189
QY	21	CysLysAsnGlnCysIleArgLeuGluLysAlaArgHISgLYserCysAsnTyr***Phe	40
DB	190	TGCAAGAATCAGTCATTAGACTTTGAGAAAGCAGACATGGATCTTGCAACTATGTCCTC	249
QY	41	ProAlaHisLysCysIleCysTyrPheProCys	51
DB	250	CCAGCTCACAGTGTATCTGCTACTTTCCTTGT	282

## RESULT 5

US-08-777-192-58  
; Sequence 58, Application US/08777192  
; Patent No. 5824869  
; GENERAL INFORMATION:  
; APPLICANT: BROEKART, WILLEM F.  
; APPLICANT: CAMMUE, BRUNO P.A.  
; APPLICANT: OSBORN, RUPERT W.  
; APPLICANT: REES, SARAH B.  
; APPLICANT: TERRAS, FRANKY R.G.  
; APPLICANT: VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BIOCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/777,192  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 06/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 43..282  
US-08-777-192-58

Alignment Scores:  
Pred. No.: 4,93e-28 Length: 288  
Score: 291.00 Matches: 47  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-777-192-58 (1-288)

QY	1	GlnLysLeuCys***ArgProSer***ThrTpSerGlyValCys***AsnAsnAsnAla	20
DB	130	CAGAAGTTGTGCCAAGGCCAAGTGGGACATGTCAGGAGTCTGTGGAAACAATAACGCA	189
QY	21	CysLysAsnGlnCysIleArgLeuGluLysAlaArgHISgLYserCysAsnTyr***Phe	40
DB	190	TGCAAGAATCAGTCATTAGACTTTGAGAAAGCAGACATGGATCTTGCAACTATGTCCTC	249
QY	41	ProAlaHisLysCysIleCysTyrPheProCys	51
DB	250	CCAGCTCACAGTGTATCTGCTACTTTCCTTGT	282

## RESULT 6

US-08-971-982-58  
; Sequence 58, Application US/08971982  
; Patent No. 6187904  
; GENERAL INFORMATION:  
; APPLICANT: BROEKERT, WILLEM F.  
; CAMMUE, BRUNO P.A.  
; OSBORN, RUPERT W.  
; REES, SARAH B.  
; TERRAS, FRANKY R.G.  
; VANDERLEYDEN, JOZEF  
; TITLE OF INVENTION: BICCIDAL PROTEINS  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CUSHMAN DABY & CUSHMAN  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/971,982  
; FILING DATE: 17-NO. 6187904-1997  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/002,480  
; FILING DATE: 04-JAN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KOKULIS, PAUL N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; INFORMATION FOR SEQ ID NO: 58:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 288 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURES:  
; NAME/KEY: CDS  
; LOCATION: 43..282  
; SEQUENCE DESCRIPTION: SEQ ID NO: 58:  
US-08-971-982-58

Alignment Scores:  
Pred. No.: 4 93e-28 Length: 288  
Score: 291.00 Matches: 47  
Percent Similarity: 100.00% Conservative: 4  
Best Local Similarity: 92.16% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-971-982-58 (1-288)

QY	1	GLNLYSLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla	20
DB	130	CAGAAGTTGTCACAAAGGCGCAAGTGGACATGTCAGGAGTCTGTGGAAACCAATACCGCA	189
QY	21	CysLYsAsnGlnCysIleArgLeuGluLYsAlaArgHisGlySerCysAsnTyr***Phe	40
DB	190	TGCAAGATCAGTGCATTAGATTGAGAAAGCAGCATGGATCTTGCACATATGTCCTTC	249
QY	41	ProAlaHisLYsCysIleCysTyrPheProCys	51
DB	250	CCAGCTCACAAAGTGTATCTGCTACTTTCCTTGT	282

## RESULT 7

US-08-627-706-16  
; Sequence 16, Application US/08627706  
; Patent No. 5773696  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Jihong  
; APPLICANT: Shah, Dilip M.  
; APPLICANT: Wu, Yonnie S.  
; APPLICANT: Rosenberger, Cindy A.  
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F  
; STREET: 700 Chesterfield Village Parkway No. 5773696th  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63198  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/627,706  
; FILING DATE:  
; CLASSIFICATION: 436  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cohen, Charles E.  
; REGISTRATION NUMBER: 34,565  
; REFERENCE/DOCKET NUMBER: 38-21(10700)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)537-6224  
; TELEFAX: (314)537-6047  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 285 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic DNA"  
US-08-627-706-16

Alignment Scores:  
Pred. No.: 2 06e-27 Length: 285  
Score: 286.00 Matches: 46  
Percent Similarity: 98.04% Conservative: 4  
Best Local Similarity: 90.20% Mismatches: 1  
Query Match: 98.28% Indels: 0  
DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-627-706-16 (1-285)

QY	1	GLNLYSLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla	20
DB	118	CAAAAGTTGTCGAGAGAGCCATCAGGACCTTGTCAGGAGTCTGCGGAAACACACACGCA	177
QY	21	CysLYsAsnGlnCysIleArgLeuGluLYsAlaArgHisGlySerCysAsnTyr***Phe	40
DB	178	TGCAAGAACCAATGCATCAACCTCGAGAAGCGACGGCATGGATCTTGCACATACGCTTTC	237
QY	41	ProAlaHisLYsCysIleCysTyrPheProCys	51
DB	238	CCAGCTCACAAAGTGCATCTGCTACTTTCATGC	270

## RESULT 8

US-09-103-489-16  
; Sequence 16, Application US/09103489  
; Patent No. 6215048  
; GENERAL INFORMATION:

APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide and Methods for  
TITLE OF INVENTION: Controlling Plant Pathogenic Fungi  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Charles E. Cohen, Monsanto Company, B44F  
STREET: 700 Chesterfield Village Parkway No. 6215048th  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63198

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
FILING DATE: 24-JUN-1998  
CLASSIFICATION: 800  
ATTORNEY/AGENT INFORMATION:  
NAME: Cohen, Charles E.  
REGISTRATION NUMBER: 34,565  
REFERENCE/DOCKET NUMBER: 38-21 (10700)A  
TELEPHONE: (314) 537-6224  
TELEFAX: (314) 537-6047  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 285 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic DNA"

US-09-103-489-16

Alignment Scores:  
Pred. No.: 2,068-27 Length: 285  
Score: 286.00 Matches: 46  
Percent Similarity: 98.04% Conservative: 4  
Best Local Similarity: 90.20% Mismatches: 1  
Query Match: 98.28% Indels: 0  
DB: 3 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-103-489-16 (1-285)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTyrSerGlyValCys\*\*\*AsnAsnAsnAla 20  
Db 118 CAAAAGTTGTGGAGAGGCCATCAGGAGCTTGGTCAGGAGTCTGGGAAACAAACACGCA 177  
QY 21 CysLysAsnGlnCysTleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
Db 178 TCGAAGAACCAATGATCATCACTCGAGAGGACGCGCATGGATCTTGCACTACGCTCTTC 237  
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
Db 238 CCAGCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 9

US-09-829-381D-16  
Sequence 16, Application US/09829381D  
Patent No. 6653280  
GENERAL INFORMATION:  
APPLICANT: Liang, Jihong  
APPLICANT: Shah, Dilip M.  
APPLICANT: Wu, Yonnie S.  
APPLICANT: Rosenberger, Cindy A.  
TITLE OF INVENTION: Antifungal Polypeptide ALYAPP from Alyssum and Methods for Control  
TITLE OF INVENTION: Plant Pathogenic Fungi

FILE REFERENCE: 38-21 (10700) C  
CURRENT APPLICATION NUMBER: US/09/829,381D  
PRIOR FILING DATE: 2001-04-09  
PRIORITY APPLICATION NUMBER: 09/103,489  
PRIOR FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 16  
LENGTH: 285  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic  
US-09-829-381D-16

Alignment Scores:  
Pred. No.: 2,068-27 Length: 285  
Score: 286.00 Matches: 46  
Percent Similarity: 98.04% Conservative: 4  
Best Local Similarity: 90.20% Mismatches: 1  
Query Match: 98.28% Indels: 0  
DB: 4 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-09-829-381D-16 (1-285)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTyrSerGlyValCys\*\*\*AsnAsnAsnAla 20  
Db 118 CAAAAGTTGTGGAGAGGCCATCAGGAGCTTGGTCAGGAGTCTGGGAAACAAACACGCA 177  
QY 21 CysLysAsnGlnCysTleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
Db 178 TCGAAGAACCAATGATCATCACTCGAGAGGACGCGCATGGATCTTGCACTACGCTCTTC 237  
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
Db 238 CCAGCTCACAAGTGCATCTGCTACTTTCATGC 270

RESULT 10

US-08-377-687-48  
Sequence 48, Application US/08377687  
Patent No. 5538525  
GENERAL INFORMATION:  
APPLICANT: BROEKERT, WILLEM F.  
APPLICANT: CAMMUE, BRUNO P.A.  
APPLICANT: OSBORN, RUPERT W.  
APPLICANT: REES, SARAH E.  
APPLICANT: TERRAS, FRANKI R.G.  
APPLICANT: VANDERLEYDEN, JOZEF  
TITLE OF INVENTION: BIOCIDAL PROTEINS  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CUSHMAN DARRY & CUSHMAN  
STREET: 1100 NEW YORK AVENUE, N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/377,687  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/002,480  
FILING DATE: 04-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KOKULIS, PAUL N.  
REGISTRATION NUMBER: 16,773  
REFERENCE/DOCKET NUMBER: 99042/SBE.36525/US/A

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEFAX: 202-822-0944  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 414 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdna  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 16..255  
 US-08-377-687-48

Alignment Scores:  
 Pred. No.: 3.45e-27 Length: 414  
 Score: 286.00 Matches: 46  
 Percent Similarity: 98.04% Conservative: 4  
 Best Local Similarity: 90.20% Mismatches: 1  
 Query Match: 98.28% Indels: 0  
 DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-377-687-48 (1-414)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAenAala 20  
 DB 103 CAGAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATATACGCA 162  
 QY 21 CysLysAsnGlnCysLeuArgLeuGlnLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 DB 163 TGAAGAATCAGTGCATTACCTTGAGAAAGCAGCATGGATCTTGCACCTATGTCCTC 222  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 DB 223 CCAGCTCACAGTGTATCTGCTACTTCTCTGT 255

# RESULT 11

US-08-777-192-48  
 Sequence 48, Application US/08777192  
 Patent No. 5824869  
 GENERAL INFORMATION:  
 APPLICANT: BROEKAERT, WILLEM F.  
 APPLICANT: CAMMUE, BRUNO P.A.  
 APPLICANT: OSBORN, RUPERT W.  
 APPLICANT: REES, SARAH B.  
 APPLICANT: TERRAS, FRANKY R.G.  
 APPLICANT: VANDERLEYDEN, JOZEF  
 TITLE OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION NUMBER: US/08/777,192  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/002,480  
 FILING DATE: 04-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEFAX: 202-822-0944  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 414 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cdna  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 16..255  
 US-08-777-192-48

Alignment Scores:  
 Pred. No.: 3.45e-27 Length: 414  
 Score: 286.00 Matches: 46  
 Percent Similarity: 98.04% Conservative: 4  
 Best Local Similarity: 90.20% Mismatches: 1  
 Query Match: 98.28% Indels: 0  
 DB: 1 Gaps: 0

SEQ9-X-AT-5-9-16-39 (1-51) x US-08-777-192-48 (1-414)

QY 1 GlnLysLeuCys\*\*\*ArgProSer\*\*\*ThrTrpSerGlyValCys\*\*\*AsnAsnAenAala 20  
 DB 103 CAGAGTTGTGCGAAGGCCAAGTGGACATGTCAGGAGTCTGTGGAAACATATACGCA 162  
 QY 21 CysLysAsnGlnCysLeuArgLeuGlnLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 DB 163 TGAAGAATCAGTGCATTACCTTGAGAAAGCAGCATGGATCTTGCACCTATGTCCTC 222  
 QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51  
 DB 223 CCAGCTCACAGTGTATCTGCTACTTCTCTGT 255

# RESULT 12

US-08-971-982-48  
 Sequence 48, Application US/08971982  
 Patent No. 6187904  
 GENERAL INFORMATION:  
 APPLICANT: BROEKAERT, WILLEM F.  
 APPLICANT: CAMMUE, BRUNO P.A.  
 APPLICANT: OSBORN, RUPERT W.  
 APPLICANT: REES, SARAH B.  
 APPLICANT: TERRAS, FRANKY R.G.  
 APPLICANT: VANDERLEYDEN, JOZEF  
 TITLE OF INVENTION: BIOCIDAL PROTEINS  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CUSHMAN DAREY & CUSHMAN  
 STREET: 1100 NEW YORK AVENUE, N.W.  
 CITY: WASHINGTON  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION NUMBER: US/08/971,982  
 FILING DATE: 17-NOV-1997  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/002,480  
 FILING DATE: 04-JAN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, PAUL N.  
 REGISTRATION NUMBER: 16,773  
 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..255
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-08-971-982-48

Alignment Scores:
Pred. No.: 3,45e-27 Length: 414
Score: 286.00 Matches: 46
Percent Similarity: 98.04% Conservatives: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 3 Gaps: 0

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Qy 1 GlnLysLeuCys***ArgProSer***ThrTrpSerGlyValCys***AsnAsnAsnAla 20
Db 103 CAGAAGTTGTGCGAAAGCCCAAGTGGGACATGCTGAGAGTCTGTGGAACAATAACGCA 162
Qy 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 163 TCGAAGATCATGTCATTAACTTGAGAAAGCAGACATGATCTTGCACACTATGCTTTC 222
Qy 41 ProAlaHisLysCysIleCysTyPheProCys 51
Db 223 CCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 14
US-09-077-948A-45
; Sequence 45, Application US/09077948A
; Patent No. 6605698
; GENERAL INFORMATION:
; APPLICANT: Van Amerongen, Aart
; APPLICANT: Fant, Franky
; APPLICANT: Borremans, Frans
; APPLICANT: De Samblanx, Geneveva
; APPLICANT: Sitjsma, Lolke
; APPLICANT: Meloen, Robbert
; APPLICANT: Puijk, Wouter
; APPLICANT: Schaaper, Wilhelmus
; APPLICANT: Broekaert, Willem
; APPLICANT: Van Gelder, Wilhelmus
; APPLICANT: Rees, Sarah
; TITLE OF INVENTION: Antifungal Proteins
; FILE REFERENCE: 109846-257(SYN-035)
; CURRENT APPLICATION NUMBER: US/09/077,948A
; CURRENT FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: PCT/GB96/03069
; PRIOR FILING DATE: 1996-12-12
; PRIOR APPLICATION NUMBER: GB 9606552.9
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: GB 9525455.3
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-09-077-948A-45

Alignment Scores:
Pred. No.: 3,45e-27 Length: 414
Score: 286.00 Matches: 46
Percent Similarity: 98.04% Conservatives: 4
Best Local Similarity: 90.20% Mismatches: 1
Query Match: 98.28% Indels: 0
DB: 4 Gaps: 0

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Db 103 CAGAAGTTGTGCGAAAGCCCAAGTGGGACATGCTGAGAGTCTGTGGAACAATAACGCA 162
Qy 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTy***Phe 40
Db 163 TCGAAGATCATGTCATTAACTTGAGAAAGCAGACATGATCTTGCACACTATGCTTTC 222
Qy 41 ProAlaHisLysCysIleCysTyPheProCys 51
Db 223 CCAGCTCAAGTGTATCTGCTACTTTCCTTGT 255

RESULT 15
US-08-627-706-5
; Sequence 5, Application US/08627706
; Patent No. 5773696
; GENERAL INFORMATION:
; APPLICANT: Liang, Jihong

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; APPLICANT: Shah, Dilip M.
; APPLICANT: Wu, Yonnie S.
; APPLICANT: Rosenberger, Cindy A.
; TITLE OF INVENTION: Antifungal Polypeptide and Methods for
; TITLE OF INVENTION: Controlling Plant Pathogenic Fungi
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles E. Cohen, Monsanto Company, BB4F
; STREET: 700 Chesterfield Village Parkway No. 5773696th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/627,706
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Cohen, Charles E.
; REGISTRATION NUMBER: 34,565
; REFERENCE/DOCKET NUMBER: 38-21(10700)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-627-706-5

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Score:          269.00      Matches:      43
Percent Similarity: 94.12%      Conservative: 5
Best Local Similarity: 84.31%      Mismatches: 3
Query Match:      92.44%      Indels:      0
DB:               1          Gaps:      0

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Qy      21  CysLysAsnGlnCysLeuArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
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Qy      41  ProAlaHisLysCysValCysTyrPheProCys 51
Db      276 CCAGCTCACAAGTGCAATATGCTACTTCCCTGT 308

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Search completed: March 24, 2004, 07:42:49  
Job time : 92 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model  
Run on: March 24, 2004, 04:48:26 ; Search time 2998 Seconds  
(without alignments)  
737.323 Million cell updates/sec

Title: SEQ9-X-AT-5-9-16-39  
Perfect score: 231  
Sequence: 1 QKLCXRPSTWGSVCXNNNA.....RHGSCNYXPPAHKICICYFPC 51

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb.ph.\*  
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9: gb.pr.\*  
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12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
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26: em.ro.\*  
27: em.sts.\*  
28: em.un.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	291	100.0	285	6	AR014693	AR014693 Sequence
2	291	100.0	285	6	AR432393	AR432393 Sequence
3	291	100.0	288	6	A39553	A39553 Sequence 41
4	291	100.0	288	6	AR050161	AR050161 Sequence
5	291	100.0	288	6	AR130280	AR130280 Sequence
6	291	100.0	288	6	I23736	I23736 Sequence 58
7	291	100.0	434	6	BD223242	BD223242 Method of
8	291	100.0	437	6	BD223241	BD223241 Method of
9	291	100.0	443	6	BD223240	BD223240 Method of
10	291	100.0	446	6	BD223239	BD223239 Method of
11	291	100.0	449	6	E34290	E34290 Phage and p
12	291	100.0	457	8	RSU18556	U18556 Raphanus sa
13	291	100.0	485	6	BD223243	BD223243 Method of
14	291	100.0	485	6	BD223245	BD223245 Method of
15	291	100.0	485	6	BD223247	BD223247 Method of
16	291	100.0	488	6	BD223248	BD223248 Method of
17	291	100.0	522	6	BD223233	BD223233 Method of
18	291	100.0	534	6	BD240936	BD240936 Polynucle
19	291	100.0	534	6	BD223234	BD223234 Method of
20	291	100.0	534	6	BD223237	BD223237 Method of
21	291	100.0	557	6	BD223246	BD223246 Method of
22	291	100.0	575	6	BD223249	BD223249 Method of
23	291	100.0	606	6	BD223236	BD223236 Method of
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28	286	98.3	395	8	RSU18557	U18557 Raphanus sa
29	286	98.3	414	6	A26875	A26875 R.sativus A
30	286	98.3	414	6	A39549	A39549 Sequence 37
31	286	98.3	414	6	A63404	A63404 Sequence 19
32	286	98.3	414	6	AR050153	AR050153 Sequence
33	286	98.3	414	6	AR130272	AR130272 Sequence
34	286	98.3	414	6	I23728	I23728 Sequence 48
35	286	98.3	414	6	AR207337	AR207337 Sequence
36	286	98.3	414	6	AR374914	AR374914 Sequence
37	281	96.6	243	6	AX412406	AX412406 Sequence
38	281	96.6	243	6	AX412601	AX412601 Sequence
39	281	96.6	243	6	AX651878	AX651878 Sequence
40	281	96.6	243	8	AY060506	AY060506 Arabidops
41	281	96.6	403	6	A68645	A68645 Sequence 13
42	281	96.6	403	8	ATANTSPC	X91916 A.thaliana
43	281	96.6	425	8	AY052236	AY052236 Arabidops
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DEFINITION Sequence 17 from patent US 5773696.
ACCESSION AR014693
VERSION AR014693.1 GI:3972147
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 5773696-A 17 30-JUN-1998;
FEATURES
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Location/Qualifiers
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Score: 291.00 Matches: 47
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Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
Db 118 CAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGCAGAGACCAATGCATCAGACTCGAGAGGACGCGCATGGATCTTGCACATACGCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270

RESULT 2
AR432393
LOCUS AR432393 285 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6653280.
ACCESSION AR432393
VERSION AR432393.1 GI:40194670
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide alyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
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DB: 6 Gaps: 0

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QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGCAGAGACCAATGCATCAGACTCGAGAGGACGCGCATGGATCTTGCACATACGCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
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RESULT 2
AR432393
LOCUS AR432393 285 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6653280.
ACCESSION AR432393
VERSION AR432393.1 GI:40194670
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 285)
AUTHORS Liang,J., Shah,D.M., Wu,Y.S. and Rosenberger,C.A.
TITLE Antifungal polypeptide alyAPP from Alyssum and methods for controlling plant pathogenic fungi
JOURNAL Patent: US 6653280-A 17 25-NOV-2003;
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Query Match: 100.00% Indels: 0
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QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
Db 118 CAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGCAGAGACCAATGCATCAGACTCGAGAGGACGCGCATGGATCTTGCACATACGCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 238 CCAGCTCACAAGTGCATCTGCTACTTCCATGC 270
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QY 1 GlnLysLeuCys**ArgProSer**ThrTpSerGlyValCys**AsnAsnAla 20
Db 118 CAAAGTTGTGCCAAGGCCATCAGGACTTGGTCAGGAGTCTGGGAAACACACGCA 177
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 178 TGCAGAGACCAATGCATCAGACTCGAGAGGACGCGCATGGATCTTGCACATACGCTTC 237
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
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RESULT 3
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LOCUS A39553 288 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 41 from Patent WO9416076.
ACCESSION A39553
VERSION A39553.1 GI:2295844
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 288)
AUTHORS Dubock,A.C., Powell,K.A. and Rees,S.B.
TITLE ANTIMICROBIAL-PROTEIN-PRODUCING ENDOSYMBIOTIC MICROORGANISMS
JOURNAL Patent: WO 9416076-A 41 21-JUL-1994;
COMMENT ZENECA LTD (GB)
FEATURES Other publication AU 5820494 940815.
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Location/Qualifiers
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Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

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Db 130 CAGAGTTGTGCCAAGGCCAAGTGGGACATGTCAGGAGTCTGGGAAACACATACGCA 189
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
Db 190 TGCAGAGACCAATGCATCAGACTTGCAGAGGACGCGCATGGATCTTGCACATACGCTTC 249
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
Db 250 CCAGCTCACAAGTGCATCTGCTACTTCCITGT 282

RESULT 4
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LOCUS AR050161 288 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 58 from patent US 5824869.
ACCESSION AR050161
VERSION AR050161.1 GI:5972153
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 288)
AUTHORS Broekaert,W.F., Cammue,B.P.A., Osborn,R.W., Rees,S.B.,
TITLE Terras,F.R.G. and Vanderleyden,J.
JOURNAL Biocidal proteins
FEATURES Patent: US 5824869-A 58 20-OCT-1998;
Location/Qualifiers
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LOCUS

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Percent Similarity:	100.00%	Conservative: 4
Best Local Similarity:	122.16%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	6	Gaps: 0

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RESULT 10
BD223239
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Artificial Sequence
PN JP 2002523047-A/8
PD 30-JUL-2002
PF 17-AUG-1999 JP 2000566429
PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI
WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE
AUGUSTINE FRANCOIS,
PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI
ANTHONY RAY
PC C12N15/09,A01H1/00,C07K1/12,C12N5/10,C12P21/02// (C12N5/10, PC
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QY 21 CysLysAsnGlnCysIleAtgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
342 TGCAGAGATCATGTCATAGACTTGCAGAAAGCACACATGATGCTTCAACTATCGTTTC 401
QY 41 ProLatisLysCysIleCysTyrPheProCys 51
402 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 434
RESULT 11
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LOCUS
DEFINITION
Phage and plasmid constructed by ligating antibacterial protein
gene DNA with vector DNA, transformant microorganism and
transformant plant containing the same and antibacterial protein.
E34290
ACCESSION
E34290.1 GI:18624295
VERSION
KEYWORDS
JP 2000116379-A/1.
SOURCE
unidentified
ORGANISM
unclassified.
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Shoji, K.
Phage and plasmid constructed by ligating antibacterial protein
gene DNA with vector DNA, transformant microorganism and
transformant plant containing the same and antibacterial protein
Patent: JP 2000116379-A 1 25-APR-2000;
TOYAMA PREF
OS Raphanus sativus L.
PN JP 2000116379-A/1
PD 25-APR-2000
PF 09-OCT-1998 JP 1998288472
PR KAZUAKI SHOJI
PI C12N15/09,A01H5/00,C07K14/415,C12N1/21,C12N5/10// PC
(C12N15/09,C12R1:91), (C12N1/21,C12R1:19), (C12N5/10,C12R1:91), PC
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Pred No.: 8,52e-25 Length: 449
Score: 291.00 Matches: 47
Percent Similarity: 100.00% Conservative: 4
Best Local Similarity: 92.16% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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128 CAGAAAGTTGTGTGCAGAGGCCAAGTCGGACATGGTCAGAGTCTGTGGAAACAATAACGCA 187
QY 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr***Phe 40
188 TGCAGAAATCATGTCATTCGACTTCAGAAAGCACACATGGTCTTGCACACTATGCTTC 247
QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51
248 CCAGCTCACAGTGTATCTGTTATTCCTTGT 280
RESULT 12
RSU18556
LOCUS
DEFINITION
Raphanus sativus antifungal protein 2 preprotein (Rs-AFP2) mRNA,
complete cds.
ACCESSION
VERSION
UI8556.1 GI:609319
SOURCE
KEYWORDS
ORGANISM
Raphanus sativus (radish)
Raphanus sativus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Raphanus.
1 (sites)
Terras,F.R.G., Eggermont,K., Kovaleva,V., Raikhel,N.V.,
Osborn,R.W., Kester,A., Rees,S.B., Torrekens,S., Van Leuven,F.,
Vanderleyden,J., Cammue,B.P.A. and Broekaert,W.F.
Small cysteine-rich antifungal proteins from radish: their role in
host defense
Plant Cell 7, 568-573 (1995)
2 (bases 1 to 457)
Terras,F.R.
Direct Submission
Submitted (14-DEC-1994) Franky R. Terras, F.A. Janssens Laboratory

```

of Genetics, Applied Biological Sciences, W. De Croylaan 42,  
Heverlee, Belgium, B-3001

Location/Qualifiers

1. .457

/organism="Raphanus sativus"

/mol\_type="mRNA"

/strain="ronde rode kleine witpunt"

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/tissue\_type="seed"

1. .457

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42. .284

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/db\_xref="GI:609320"

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42. .128

/genes="Rs-APP2"

129. .281

/genes="Rs-APP2"

/products="antifungal protein 2"

/function="antifungal, fungistatic"

/note="Evidence for antifungal activity: Analysis of two novel classes of antifungal proteins from radish (Raphanus sativus L.) seeds. Terras, F.R.G. et al. (1992), J. Biol. Chem. 267, 15301-15309"

/citation=[1]

/evidence=experimental

ORIGIN

Alignment Scores:

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Score: 291.00 Matches: 47

Percent Similarity: 100.00% Conservative: 4

Best Local Similarity: 92.16% Mismatches: 0

Query Match: 100.00% Indels: 0

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Db 129 CAGAAGTTGTGCAGAGGCCAAGTGGGCACATGTCAGAGCTCTGTGGAAATAATAACGCA 188

QY 21 CVELYASGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40

Db 189 TGCAGAATCAGTGCATTTCGACTTGAAAGCAGCATGGTGCTTTCGCAACTATGCTTC 248

QY 41 ProAlaHisLysCysIleCysTyrPheProCys 51

Db 249 CCAGCTCACAAGTGATCTCTGTTATTCCTTGT 281

RESULT 13

BD223243

LOCUS

BD223243

DEFINITION

Method of genetic expression of polyprotein in plant.

BD223243

ACCESSION

BD223243.1 GI:33033013

VERSION

JP 2002523047-A/12.

KEYWORDS

synthetic construct

SOURCE

synthetic construct

ORGANISM

artificial sequences.

REFERENCE

1 (bases 1 to 485)

Broekaert, W.F., Francoijs, I.E.J.A., Bolle, M.F.C.D., Evans, I.J. and Ray, J.A.

AUTHORS

Method of genetic expression of polyprotein in plant

TITLE

JOURNAL

Patent: JP 2002523047-A 12 30-JUL-2002;

SYNGENTA LTD

Key CDS Location/Qualifiers  
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 Location/Qualifiers  
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 DB: 6 Gaps: 0

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 Db 381 TGCAGAAATCAGTGCATAGACTTGAGAAGCAGCAGATGGATCTTGCAACTATCGTTTC 440  
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 Db 441 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 473

## RESULT 15

BD223247 485 bp DNA linear PAT 17-JUL-2003  
 LOCUS  
 DEFINITION Method of genetic expression of polyprotein in plant.  
 ACCESSION BD223247  
 VERSION BD223247.1 GI:33033017  
 KEYWORDS JP 2002523047-A/16.  
 SOURCE synthetic construct  
 ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 485)  
 AUTHORS Broekaert,W.F., Francois,I.E.J.A., Bolle,M.F.C.D., Evans,I.J. and Ray,J.A.

TITLE Method of genetic expression of polyprotein in plant

JOURNAL Patent: JP 2002523047-A 16 30-JUL-2002;

COMMENT OS Artificial Sequence  
 FN JP 2002523047-A/16  
 PD 30-JUL-2002

PF 17-AUG-1999 JP 2000556429  
 PR 18-AUG-1998 GB 9818001.1,04-DEC-1998 GB 9826753.7 PI  
 WILLEM FRANS BROEKAERT, ISABELLE ELSA JEANNE  
 AUGUSTINE FRANCOIS  
 PI MIGUEL FRANCESCO COLETA DE BOLLE, IAN JEFFREY EVANS, JOHN PI  
 ANTHONY RAY  
 PC C12N15/09,A01H1/00,C07K1/12,C12N5/10,C12P21/02//C12N5/10, PC  
 C12R1:91)  
 PC C12N15/00,C12N5/00,(C12N5/00,C12R1:91)  
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FEATURES  
 source

## ORIGIN

Alignment Scores:  
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 Percent Similarity: 100.00% Conservative: 4

Best Local Similarity: 92.16% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
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 Db 321 CAGAAAGTTGTGCCAAAGGCCAAGTCGTACATGGTCAGGAGTCTGTGGAAACAATAACGCA 380  
 Qy 21 CysLysAsnGlnCysIleArgLeuGluLysAlaArgHisGlySerCysAsnTyr\*\*\*Phe 40  
 Db 381 TGCAGAAATCAGTGCATAGACTTGAGAAGCAGCAGATGGATCTTGCAACTATCGTTTC 440  
 Qy 41 ProLalaHisLysCysIleCysTyrPheProCys 51  
 Db 441 CCAGCTCACAGTGTATCTGCTACTTTCCTTGT 473

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